


```
Db 61 FKQETVTDLTGYGMEYIOGNSAENENSWTRVAFAGLKFQDVGSFDTGRNYGVYD 120
QY 121 VTSMTDVLPEFGGDTYGSDFMQRGNGFATYRNRTDFGLVDGLNFAVOYQKNGNSGE 180
Db 121 VTSMTDVLPEFGGDTYGSDFMQRGNGFATYRNRTDFGLVDGLNFAVOYQKNGNSGE 178
QY 181 GFISGVTNNGRDALRONGDVGSGITTYDEGFGIGAISSSKRPDQONTAAVYIGNDGRAE 240
Db 179 ---EGMTNNGEREARLRONGDVGSGITTYDEGFGIGAAVSSSKRTDDQNSPLYIGNDGRAE 235
QY 241 TTYGGLKYDANNIYLAAYQTYTNATPVGSLGNANKAONEEAAVOYQFDEGLRPSLAYLQ 300
Db 236 TTYGGLKYDANNIYLAAYQTYTNATPVGSLGNANKAONEEAAVOYQFDEGLRPSLAYLQ 295
QY 301 SKGKNL----GRGYDEDDILKYDVGATYTFNKNMSTYVDYKINLDDNOFTRDAGINTD 356
Db 296 SKGKNLGVINGRNYDEDDILKYDVGATYTFNKNMSTYVDYKINLDDNOFTRDAGINTD 355
QY 357 NIVALGLVYQF 367
Db 356 NIVALGLVYQF 366

RESULT 2
ID 09K597 PRELIMINARY; PRT; 364 AA.
AC 09K597;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE OUTER MEMBRANE PORIN C PRECURSOR.
GN OMP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Low A.S., Mackenzie F.M., Gould I.M., Booth I.R.;
RT "Parallel evolution of multi-resistant bacteria in a patient with
RT recurrent septicemia: unique data that support the presence of
RT separate protected environments."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
DR EMBL; AJ295721; CAC01403.1; -.
DR InterPro; IPR000504; -.
DR pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
KW Outer membrane; Porin; Signal; Transmembrane.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 364 AA; 40312 MW; 9B583FC1344E31 CRC64;

Query Match 87.5%; Score 1709.5; DB 2; Length 364;
Best Local Similarity 88.0%; Pred. No. 3,4e-113;
Matches 333; Conservative 14; Mismatches 27; Indels 3; Gaps 1;
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Db 121 VTSMTDVLPEFGGDTYGSDFMQRGNGFATYRNRTDFGLVDGLNFAVOYQKNGNSAHE 180
QY 181 GFISGVTNNGRDALRONGDVGSGITTYDEGFGIGAISSSKRTDAONTAAVYIGNDGRAE 240
Db 181 GMT---TNGRDVDFEONGDVGSGITTYDEGFGIGAAVSSSKRTDQNTNGLTGTGDRAE 237
QY 241 TTYGGLKYDANNIYLAAYQTYTNATPVGSLGNANKAONEEAAVOYQFDEGLRPSLAYLQ 300
Db 238 TTYGGLKYDANNIYLAAYQTYTNATPVGSLGNANKAONEEAAVOYQFDEGLRPSLAYLQ 297
QY 301 SKGKNLGRGYDEDDILKYDVGATYTFNKNMSTYVDYKINLDDNOFTRDAGINTDIVA 360
Db 298 SKGKNLGRGYDEDDILKYDVGATYTFNKNMSTYVDYKINLDDNOFTRDAGINTDIVA 357
QY 361 LGLVYQF 367
Db 358 LGLVYQF 364

RESULT 3
ID 09K3E6 PRELIMINARY; PRT; 378 AA.
AC 09K3E6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR.
GN OMP.
OS Salmonella enterica subsp. enterica serovar Minnesota.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=70803;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann H., Wassenaar T.M., Laubenheimer-Preusse H., Petry F.,
RA Loois M.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
DR EMBL; Y15844; CAB96613.1; -.
DR InterPro; IPR000504; -.
DR pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
KW Outer membrane; Porin; Signal; Transmembrane.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 378 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 378 AA; 41269 MW; 254524EB9EC3849C CRC64;

Query Match 78.6%; Score 1534.5; DB 2; Length 378;
Best Local Similarity 77.1%; Pred. No. 8e-101;
Matches 296; Conservative 25; Mismatches 40; Indels 23; Gaps 5;
```

QY	237	DRAEYTGGLKYDANNIYLAQYQYTNAIRYG-----SLGMANKAQNEEVAQAQY	287
Db	235	DRAATYTGGLKYDANNIYLAQAQYQYTNAIRFGTSGNKNKSDSYGEFANKAQNEEVAQAQY	294
QY	288	FDEGLRPSLATLQSKGNLGRG----DDDEILKLYVDVGATYYFNKMSYYVDKIIYLLD	343
Db	295	FDEGLRPSVAALQSKGKDINSNGYASGYDDQIVRYVDVGATYYFNKMSYYVDKIIYLLD	354
QY	344	DNQFTRDAGINTDNIIVALGLYQF	367
Db	355	KNDFTRDAGINTDNIIVALGLYQF	378

RESULT	4			
085030		PRELIMINARY;	PRT;	377 AA.
AC	085030			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
DE	PORIN OMPN.			
GN	OMP.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxId=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BE (BL21);			
RX	MEDLINE=98317278; PubMed=9642192;			
RA	Philpov A., Phale P.S., Koehnig R., Widmer C., Rosenbusch J.P.;			
RT	"Identification and characterization of two quiescent porin genes			
RT	nmpr and ompN, in Escherichia coli BE.";			
RL	J. Bacteriol. 180:3388-3392(1998).			
DR	EMBL: AF035618; AAC8644.1. -.			
DR	HSSP: P02931; IGFN			
DR	InterPro: IPR000408; -.			
DR	InterPro: IPR001702; -.			
DR	Pfam: PF00267; Gram-ve_porins; 1.			
DR	PRINTS: PR00182; ECOLIOMPORIN			
DR	PROSITE: PS00626; RCCL_2; UNKNOWN_1			
DR	SEQUENCE 377 AA; 41236 MW; F74D81A2BC10F8C CRC64;			

Query Match	66.4%;	Score 1296;	DB 2;	Length 377;
Best Local Similarly	68.1%;	Pred. No. 5.5e 84;		
Matches 262;	Conservative 36;	Mismatches 61;	Indels 26;	Gaps 10;

QY 1 MRSYVLLPALLPALLAAQAHAHAEEYKNDGKKLLDYGVDGLTFHESDPRKDVDSGQOTWRIG 60

Db 1 MRSYVLLPALLPALLAAQAHAHAEEYKNDGKKLLDYGVDGLTFHESDPRKDVDSGQOTWRIG 60

QY 61 FKGETQVTDLDTGYGOMEYIOGNSAE--NENSWTRFAVAGLKFQDYGSEFDYGRNGVY 119

Db 61 FKGETQVTDLDTGYGOMEYVNOANNTESSKQSTRTLAFAGLKFADYGSFDYGRNGVY 120

QY 120 DVTSMITVLPFEGGDDY--GSPNFQMGQNGGATYRTNDFEGLVDGLNFAAYOYGGKGNPS 178

Db 121 DTEGHTDMLPEFGSDSTYNADNFEPTGANGAVYIYRTNDFEGLVNGLNFAYOYGGN---- 176

QY 179 GEGFTSGV--TNNGRDALRONGDVGSGSYTDY--EGFGIGAISSSKRTDAQ--NTAAVY 233

Db 177 -EGASNGCEGTNNGRDVRHENGSDMGWSTTYDLDLGMGSAQAATYSTSDPTNDQVNH7AA-- 233

QY 234 GNGRAEETVTEGLKYDDANNYYLAAQYQYTNAPRVGSLG-- -NNKQNFPAVAQYOEDG 291

Db 234 -GGGRADMTWTEGLKYDDANNYYLAMYSETRNMPFEGSDYAVANKQNFYEV7AQYQEDG 292

QY 292 LRPSLAYIQSGKKVL-----GRGYDDEDLKYVDVGATYYFNKKNMSTVYDYKTNLND 343

Db 293 LRPAVSELMSSGRDLHAAGGADNPAGVDDDLVLYADVGATYYFNKKNMSTVYDYKTNLND 352b

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QY      344 -DNQETRDAGINTDNIVALGLVYQF 367
      | : | | : | : | | | | | | | |
Db      353 EDDSFYTANGISTDDIVALGLVYQF 377
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RESULT	5			
ID	087754	PRELIMINARY;	PRT;	374 AA.
AC	087754;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	OMP37 PORIN PRECURSOR.			
GN	OMP37.			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
CC	Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SD8;			
RA	Domenech-Sanchez A., Hernandez-Alles S., Martinez-Martinez L.,			
RT	Benedi V.J., Alberti S. "Identification and characterization of a novel porin of Klebsiella			
RL	pneumoniae: its role in beta-lactam antibiotics resistance.";			
DR	Submitted (SEP-1998) to the EMBL/Genbank/DBD databases.			
DR	HML; AJ011502; CAA09666.1; -.			
DR	HSSP; Q48473; IOSM.			
DR	InterPro; IPR000408; -.			
DR	InterPro; IPR001702; -.			
DR	Pfam; PF00267; Gram-ve_porins; 1.			
DR	PRINTS; PR00182; ECOLEI00RN.			
DR	PROSITE; PS00626; RCCL_2; UNKNOWN_1.			
FT	SIGNAL.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	374	OMP37 PORIN.
SQ	SEQUENCE	374 AA;	41612 MW;	B66DFDD74A1A169B CRC64;

Query Match	64.0%;	Score 1250.5;	Length 374;
Best Local Similarly	66.0%;	Pred. No. 8.8e-81;	
Matches 249; Conservative	44;	Mismatches 71;	Indels 13; Gaps 10;

[illegible]

RESULT 6

09K3E7 PRELIMINARY; PRT; 363 AA.
 ID 09K3E7
 AC 09K3E7
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE OUTER MEMBRANE PROTEIN FX PRECURSOR.
 OMPEX.
 OS Salmonella enterica subsp. enterica serovar Minnesota.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxId=70803;
 OX NCBI_TaxId=70803;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SE111;
 RA Zimmermann H., Wassenaar T.M., Laubenheimer-Preusse H., Petry F.,
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y15843; CAB9614.1; -
 DR InterPro: IP001702; -
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOINELPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; UNKNOWN_1.
 DR SIGNAL.
 KW Signal.
 FT CHAIN 23 363 OUTER MEMBRANE PROTEIN FX.
 FT SEQUENCE 363 AA; 40090 MW; F5058DEDA516859 CRC64;
 SQ SEQUENCE

Query Match 52.5%; Score 1025.5; DB 2; Length 363;
 Best Local Similarity 53.2%; Pred. No. 6.5e-65;
 Matches 201; Conservative 60; Mismatches 90; Indels 27; Gaps 7;

1 MKKVALIIPALLAAGAAHAEEVYNKDKKLDLYGVDELHFEPSDKD-VDDDOTYMR 59
 2 MKKKILAAVTPALLAATAAATAAETYNKDKKLDLYGAVRHWATTTGDSKNADQY 61
 60 GFGGETVDLTGYGWEYIOGNSAENE--NSWTRVAFAGLKFDQVGSFPGYRNYG 117
 62 GFGGEGQINTDLGFGQWEVTRKADRAEGEQNSNLVRLAFAGLKAYEVSIDYGRNY 121
 118 VYVYTSKTDVLPFEGGDTYV---SDNFMQORGNFATYRNTDFEGLVDGINFAVOY 174
 122 VYDVESYTDAPYFSGTNGCATYTDNMTSRACGLLTRYNSDFEGLVDGSLFIQY 181
 175 GNSGGEFTSGVNNNGDALRONGDVGSGITDYDEFGIGCAISSKRRDAQNTA 234
 182 -----QDNHSINSQNGDVGTYMAVEFDGFGVTAAYSNSKRTNDQD 226
 235 NGDRAETYGTLKYDANNITLAAQYOTYNA-----TRVSLGMANKQNEVA 289
 227 NGDRAESMAVGAKYDANNYLAAYVATETRMSTYVENTYDTFEMANKTQVLE 286
 290 FGLRPSLAIVLQSKGNLGRGVDDEDLIKYVDVATYFENKMSYTYDYKINLLD 349
 287 FGLRPAISYVQSKQNLGADSGADSLAKYIQAGATYFENKMNVMWVDYRNL 345
 350 DAGINTDNIVALLGYQF 367
 346 SSTYGTVDVAAGVITYQF 363

RESULT 7
 09RAM3 PRELIMINARY; PRT; 333 AA.
 AC 09RAM3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PHOSPHATE PORIN (FRAGMENT).
 GN PHOE.
 OS Klebsiella pneumoniae (subsp. ozaenae).
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.
 OX NCBI_TaxId=574;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=I436;
 RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Striprakash K.S.,
 RT Kemp D.J.;
 CC "Phylogenetic analysis of Calymmatobacterium granulomatis."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT. HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
 (BY SIMILARITY).
 CC EMBL; AF009229; AAD21517.1; -
 DR HSSP; P02932; LPHO.
 DR InterPro: IP001702; -
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOINELPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Porin; Signal; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 333 333
 SQ SEQUENCE 333 AA; 36839 MW; 68AF347207770ABA CRC64;

Query Match 52.2%; Score 1018.5; DB 2; Length 333;
 Best Local Similarity 56.5%; Pred. No. 1.8e-64;
 Matches 200; Conservative 53; Mismatches 76; Indels 25; Gaps 8;

8 LILPALLAAGAAHAEEVYNKDKKLDLYGVDELHFEPSDKDQVDDQTYMRGFGKET 67
 1 LMMKGFVASTATDAAEYNNKANKLDLYGKIKAMHYFSDSKDQDYVRFGIKGT 60
 68 TDULTGYGWEYIOGNSAENNSWTRVAFAGLKFDQVGSFPGYRNYGVYVYTSMT 127
 1 NDULTGGRWSEFSFGKRTSDSSQKTRLAFAVGLKATNGSPYGRNLALYVEAMTD 120
 128 LPFEGGDTYV-SDNFMQORGNFATYRNTDFEGLVDGLNFAVOYQKNCNP 186
 121 FPFEGDSSAQOTDNFMTKRSAGLATYRNTDFEGLVDGLDITLYQK----- 167
 187 TNGRDLRONGGVGSGITYDEG--FGIGCAISSKRRDAQNTAAYIGNGRAET 244
 168 -NGGRKAKKONGGVGSGTSLYDGGDFVAAYTSSDRTNDQNLAR-GQGSKA 225
 245 GLKYDANNITLAAQYOTYATVATRGVSLGMANKQNEVAVAQYDFGLRPSLA 304
 226 GLKYDANNITLAAQYOTYATVATRGVSLGMANKQNEVAVAQYDFGLRPSLA 284
 305 NLGRGYDDEDILKYVDVATYFENKMSYTYDYKIN-LDDNOFTRDAGINTDN 357
 285 DI-EGVGSDELIVYIDVGLTYRNNKMNNAFVDYKINQKLSDNKL----- 333

RESULT 8
 09RAM2 PRELIMINARY; PRT; 333 AA.
 AC 09RAM2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PHOSPHATE PORIN (FRAGMENT).
 GN PHOE.
 OS Klebsiella pneumoniae subsp. rhinoscleromatis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxId=39831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIC5046;
 MEDLINE=20023050; PubMed=1055350;
 RX Carter J.S., Bowden F.J., Bastian I., Myers G.M., Striprakash K.S.,
 RA Kemp D.J.;
 RT "Phylogenetic evidence for reclassification of Calymmatobacterium

OY 354 NMDNVALGLYOF 367
 Db 346 ATDDAAVGIYOF 359

RESULT 13

O9EXH8 PRELIMINARY; PRT: 315 AA.
 AC O9EXH8;
 DT 01-MAR-2001 (Tremblrel, 16, Created)
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
 DE 01-MAR-2001 (Tremblrel, 16, Last annotation update)
 GN OMPK35 PROTEIN PRECURSOR.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-103624;
 RA Crowley B., Benedi V.J., Domenech-Sanchez A.;
 RT "Expression of altered OmpK35 porin and SHY-2 beta-lactamase in
 Klebsiella pneumoniae results in cephalosporins and carbapenems
 resistance."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ303057; CAC18650.1;
 KW SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 315 OMPK35 PROTEIN.
 SQ SEQUENCE 315 AA; 34420 MW; F45748383475D8CA CRC64;

Query Match 44.2%; Score 862.5; DB 2; Length 315;
 Best Local Similarity 52.9%; Pred. No. 1,7e-53;
 Matches 174; Conservative 47; Mismatches 85; Indels 23; Gaps 6;

OY 1 MRSKVLALLIPALLAAGAAHAEVYNRKDKNLIDYKVDGLHYPSPDKDVGDDQ-TYMR 59
 Db 2 MKRNILAVIIPALLVAGANAAYLNKNGKLDYFGKVGSHVWTTGGDSSDPTTARI 61
 OY 60 GFKGTQVTDQLTGYGWEYQIOGNSAENENNSTRYAFAGLAFKQDYGSPDYGRNYGVY 119
 Db 62 GLKGTQINDLIGYQWEYMDASNEGSGQTTFLAFLGKAGEVSPDYGRNYGAIY 121
 OY 120 DVTSMVDLPFEGGDTYG-SDNEMQGNFGATYRNTDFGLVGLNFAVOYQKNGNPS 178
 Db 122 DVEATDMLVEMGSDGMNYTDNMTGRTNGVATYRNSDFGLVGLSFALQYQGN- 177
 OY 179 GEGTSGVTNNGRDALRQNGDVGSGITYDYE-GFGIGAISSSKRTDAONTAAYIGND 237
 Db 178 -----DHDRAIRQNGDGFSTAATYAFANDGIALSAGYSSSNRSIDQKAD---GNGD 225
 OY 238 RAETTYGGLKTDANNITLAAYOTYATNATRVGSLGMANKQNFPAVAYOYQDFGLRPSLA 297
 Db 226 KAEWMATSAKADANNITLAAYVSYQTYNMTPEEDNHFAGKTQNFPAVAYOYQDFGLRPSIG 285
 OY 298 YLQSGKNNL---GRGYDDEDIILKYDVG 322
 Db 286 YVOTKGDLOSRAFGSGDADLVKTIENG 314

RESULT 14
 O9XC71 PRELIMINARY; PRT: 315 AA.
 AC O9XC71;
 DT 01-MAY-1999 (Tremblrel, 10, Created)
 DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)
 DE SIMILAR TO OMPF.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.

OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-6/69;
 RA Buchrieser C., Rusniok C., Couve E., Frangeul L., Billault A.,
 RA Kunst F., Carniel E., Glaser P.;
 RT "DNA sequence of the 102 kbases unstable region of Yersinia pestis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL031866; CAA21336.1;
 DR HSSP: P02931; IGFN.
 DR InterPro: IPR001702;
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLNTEPORIN.
 SQ SEQUENCE 315 AA; 34304 MW; D32FB91828EDA17A CRC64;

Query Match 37.5%; Score 732; DB 2; Length 315;
 Best Local Similarity 51.5%; Pred. No. 2.8e-44;
 Matches 158; Conservative 40; Mismatches 83; Indels 26; Gaps 9;

OY 1 MRSKVLAL-----LIPALLAAGAAHAEVYNRKDKNLIDYKVDGLHYPSPDKDVGDDQ 55
 Db 1 MKNITAMLAATLGIIPAL-----SSAAEIVNKKDKNLIDYGRVAAKYLE--KKQSNEDAT 53
 OY 56 YMRIGFEGTQVTDQLTGYGWEYQIOGNSAENEN--SWTRVAFAGLAFKQDYGSPDYGR 113
 Db 54 YVRIGFEGTQVTDQLTGYGWEYQIOGNSAENEN--SWTRVAFAGLAFKQDYGSPDYGR 113
 OY 114 NYGVYVNTSWTDLPFEGGDTY-SDNEMQGNFGATYRNTDFGLVGLNFAVOYQKNGNPS 172
 Db 114 NYGVYVNTSWTDLPFEGGDTY-SDNEMQGNFGATYRNTDFGLVGLNFAVOYQKNGNPS 173
 OY 173 KGNPSEGEFTSGVTNNGRDALRQNGDVGSGITY-DYEGFGI--GGAISSSKRTDAONT 229
 Db 174 RNED-----GDVTRNERSTQKANGDGFGLSTFYQVIOGSGVFAAYSSSNTEBQKE 226
 OY 230 AAYIGNDRAETTYGGLKYDANNITLAAYOTYATNATRVGSLGMANKQNFPAVAYOYQD 289
 Db 227 LVNSAAGDKAQMAYTGKLYDANNITLAAYOTYATNATRVGSLGMANKQNFPAVAYOYQD 285
 OY 290 FGLRPSL 296
 Db 286 NGIRPSL 292

RESULT 15
 O52641 PRELIMINARY; PRT: 130 AA.
 AC O52641;
 DT 01-NOV-1996 (Tremblrel, 01, Created)
 DT 01-NOV-1996 (Tremblrel, 01, Last sequence update)
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)
 DE OMPF (FRAGMENT).
 GN OMPF.
 OS Rahnelia aquatilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Rahnelia.
 OX NCBI_TaxID=34038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CF3;
 RA Achouak W., de Mot R., Heulin T.;
 RL FEMS Microbiol. Ecol. 0:0-0(0).
 DR EMBL: U17430; AAA56871.1;
 DR HSSP: P09878; IITV.
 DR InterPro: IPR001702;
 DR Pfam: PF00267; Gram-ve_porins; 1.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 14510 MW; DB6A341744A48E5 CRC64;

Query Match 26.5%; Score 518.5; DB 2; Length 130;

Best Local Similarity 71.5%; Pred. No. 1e-29; Mismatches 18; Indels 1; Gaps 1;
Matches 93; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

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QY 23 EVYKKGDKNKLDELGYKVDGLHYFSDNKNVDGDDQTYMRLGFKGETQVTDQLTGYGOMEYQIQ 82
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EYKKGDKNKLDELGYKVDGLHYFSDNKNVDGDDQTYMRLGFKGETQVTDQLTGYGOMEYQIQ 60
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 83 GNSAENEN-NSWTPVAFAPAGLKFDVGSFEDYGRNYGVVYDVTSMTPDVLPERFGDTYGSDF 141
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LNTGESEDANNFTYRVPAGLKFQGMGSLDYGRNYGVVYDVTSMTPDVLPERFGDTYGSDF 120
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 142 MOQRNFGAT 151
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 MQRNFGAT 130
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

Search completed: August 21, 2001, 20:59:22
Job time: 97 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 13.1 Seconds

(without alignments)
959.677 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MRSKVALIPALLAAGAAH.....TRDAGINTDNIYALGLVYQF 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1	OMP_C_ECOLI
2	1539.5	78.8	378	1	OMP_C_SALTI
3	1537	78.7	363	1	OMP_C_KLEPN
4	1512.5	77.4	378	1	OMP_C_SALTY
5	1296	66.3	383	1	OMP_S_SALTY
6	1295	66.3	377	1	OMP_N_ECOLI
7	1283.5	65.7	376	1	OMP_C_SERMA
8	1241	63.5	374	1	OMP_C_SERMA
9	1220	62.5	342	1	OMP_C_RAHQ
10	1213.5	62.1	394	1	OMP_S_SALTI
11	1187	60.8	397	1	YEDS_ECOLI
12	1177	60.3	365	1	NMPC_ECOLI
13	1169	59.9	365	1	PORT_BPPAZ
14	1129.5	57.8	350	1	PHOE_ENTCL
15	1109	56.8	351	1	PHOE_ECOLI
16	1104	56.5	351	1	OMP_F_ECOLI
17	1086	55.6	351	1	PHOE_CITFR
18	1065.5	54.6	350	1	PHOE_SALTY
19	1060	54.3	349	1	PHOE_KIEOX
20	1059	54.2	351	1	PHOE_KIEPN
21	1055.5	54.0	350	1	PHOE_KLEPN
22	1029.5	52.7	363	1	OMP_F_SALTY
23	1027.5	52.6	363	1	OMP_F_SALTY
24	1002	51.3	369	1	OMP_F_XENNE
25	882	45.2	382	1	OMP_C_SALTY
26	592	30.3	382	1	PORT_BUCAI
27	289	14.8	341	1	OMP_C_PHOPR
28	279	14.3	341	1	OMP_C_VIBCH
29	196	10.0	363	1	OMP_C_HAEIN
30	194.5	10.0	367	1	OMP_C_HAEIN
31	194.5	10.0	371	1	OMP_C_HAEIN
32	192.5	9.9	361	1	OMP_C_HAEIN
33	191.5	9.8	369	1	OMP_C_HAEIN

34	189	9.7	360	1	OM26_HAEIN	Q48216 haemophilus
35	187.5	9.6	353	1	OM28_HAEIN	Q48221 haemophilus
36	176	9.0	386	1	OM24_HAEIN	P46026 haemophilus
37	174.5	8.9	326	1	OMP_C_PHOPR	P29739 photobacter
38	173.5	8.9	385	1	OM23_HAEIN	P46025 haemophilus
39	164.5	8.4	361	1	OM22_HAEIN	P20149 haemophilus
40	163.5	8.4	359	1	OM21_HAEIN	P43839 haemophilus
41	154	7.9	348	1	OM2_HAEIN	P20148 haemophilus
42	153	7.8	348	1	OM2_NEIGO	P18195 neisseria g
43	152.5	7.8	385	1	OMP_BORPE	Q04064 bordetella
44	141	7.2	351	1	OMP_COMAC	P24305 comamonas a
45	140	7.2	393	1	OM21_NEIMC	P13415 neisseria m

ALIGNMENTS

RESULT 1
OMP_C_ECOLI
ID OMP_C_ECOLI STANDARD: PRT: 367 AA.
AC P06996:
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMP_C) (OUTER MEMBRANE PROTEIN 1B).
GN OMP_C OR MECA OR PAR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83213433; PubMed=6304064;
RA Mizuno T., Chou M.-Y., Inouye M.;
RT "A comparative study on the genes for three porins of the Escherichia coli outer membrane. DNA sequence of the osmoregulated omp gene."; J. Biol. Chem. 258:6932-6940(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RA MEDLINE=9742617; PubMed=9278503;
RA Blatner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."; Science 277:1233-1238(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-K12:
RA MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H., Takada J., Takemoto K., Wada C., Yamamoto Y., Horinouchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 218-367 FROM N.A.
RX STRAIN-K12 / BHB2600;
RA Richerich P., Lahey N., Gryan G., Jaehn L., Mintz L., Robison K., Church G.M.;
RT Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-22 FROM N.A., AND SEQUENCE OF 22-40.
RX MEDLINE=83132326; PubMed=6297988;
RA Mizuno T., Chou M.-Y., Inouye M.;
RT "DNA sequence of the promoter region of the ompc gene and the amino acid sequence of the signal peptide of pro-Ompc protein of

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RT Escherichia coli."
RL FEBS Lett. 151:159-164(1983).
RN
RP SEQUENCE OF 32-57 FROM N.A.
RX MEDLINE=86033642; PubMed=2997131;
RA Nogami T., Mizuno T., Mizushima S.;
RT Construction of a series of ompF-ompC chimeric genes by in vivo
RT homologous recombination in Escherichia coli and characterization of
RT the translational products."
RL J. Bacteriol. 164:797-801(1985).
RN
RP SEQUENCE OF 22-30.
RX STRAIN-K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN
RP SEQUENCE OF 22-26.
RX STRAIN-K12 / M3110;
MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RA Sanchez J.C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT Extraction of membrane proteins by differential solubilization for
RT separation using two-dimensional gel electrophoresis."
RL Electrophoresis 19:837-844(1998).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
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DR EMBL: K00541; AAA24243.1;
DR EMBL: AE000310; AAC75275.1;
DR EMBL: D90850; BAA15988.1;
DR EMBL: U00008; AAA16412.1;
DR PIR: A20867; MMECP.
DR PIR: B25029; B25028.
DR PIR: A18885; A18885.
DR HSSP: P02931; IGFN.
DR ECO2DBASE: A035.5; 6TH EDITION.
DR EcoGene: EG10670; ompC.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram_+_porins; 1.
DR PRINTS: PR00182; ECOLIEMPORIN.
DR PRINTS: PR00183; ECOLIEMPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
FT SIGNAL 1 21
FT CHAIN 1 367
SQ SEQUENCE 367 AA; 40368 MW; 6A49370CC8A1A225 CRC64;

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Query Match 98.0%; Score 1914; DB 1; Length 367;
Best Local Similarity 98.1%; Pred. No. 7.8e-126;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MSKVALALLIPALLAAGAAHAAYNKDKGLDYGVKVDGLHFHFSNDKVDGQDTYWRIG 60
DB 1 MKKVALSLVLPALLVAGANAAYNKDKGLDYGVKVDGLHFHFSNDKVDGQDTYWRIG 60
QY 61 FKETQVTDLTGTGQWEYIOGNSAENENNSWTRVAFAGLKFQDVGSEFYGRNYGVYD 120

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DB 61 FKETQVTDLTGTGQWEYIOGNSAENENNSWTRVAFAGLKFQDVGSEFYGRNYGVYD 120
QY 121 VTSWTDVLPFGGDTYSGDNPQORNGFATYRTDFFGLVDGLNFVVOYQGNKGNPSGE 180
DB 121 VTSWTDVLPFGGDTYSGDNPQORNGFATYRTDFFGLVDGLNFVVOYQGNKGNPSGE 180
QY 181 GFTSGVTNNRDLRQNGDVGSGITVDYEGFISGAISSSKRTDAQNTAAYTGNDRAE 240
DB 181 GFTSGVTNNRDLRQNGDVGSGITVDYEGFISGAISSSKRTDAQNTAAYTGNDRAE 240
QY 241 TYTGGLKYDANNITYLAAQYQTINATRVGSLGNANKQNEAQAQYQDFGLRPSLAYLQ 300
DB 241 TYTGGLKYDANNITYLAAQYQTINATRVGSLGNANKQNEAQAQYQDFGLRPSLAYLQ 300
QY 301 SKGKNLGRGVDDEDIKYYVVGATFYFNKMSYVDYKINLLDNOFTRDAGINTDNTVA 360
DB 301 SKGKNLGRGVDDEDIKYYVVGATFYFNKMSYVDYKINLLDNOFTRDAGINTDNTVA 360
QY 361 LGLVYQF 367
DB 361 LGLVYQF 367

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RESULT 2
OMP_C_SALTI STANDARD; PRT; 378 AA.
ID OMP_C_SALTI
AC P09878;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMP_C).
GN OMP_C.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90060831; PubMed=2684785;
RA Puente J.L., Alvarez-Scherer V., Gosset G., Calva E.;
RT "Comparative analysis of the Salmonella typhi and Escherichia coli
RT ompC genes."
RL Gene 83:197-206(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-TY2;
MEDLINE=88319959; PubMed=3412902;
RA Venegas A., Gomez I., Zator I., Yudelevich A.;
RT "The nucleotide sequence of the Salmonella typhi ompC porin gene."
RL Nucleic Acids Res. 16:7721-7721(1988).
RN [3]
RP 3D-STRUCTURE MODELING AND CRYSTALLIZATION.
RX MEDLINE=99332091; PubMed=10405180;
RA Brockiasamy A., Krishnaswamy S.;
RT "Crystallization of the immunodominant outer membrane protein OmpC;
RT the first protein crystals from Salmonella typhi, a human pathogen."
RL FEBS Lett. 453:380-382(1999).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
CC -----
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DR EMBL: M31424; AAA27169.1;
DR EMBL: X07835; CAA30688.1;

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DR PIR: J00119; MMEBPC.
 DR PIR: S01248; S01248.
 DR PDB: 1IIV; 14-OCT-98.
 DR InterPro: IPR001702; -.
 DR InterPro: IPR001897; -.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLIPORIN.
 DR PRINTS: PR00183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 DR Outer membrane; Transmembrane; Porin; Phage recognition; Signal;
 KW 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 378 OUTER MEMBRANE PROTEIN C.
 FT CONFLICT 362 362 MISSING (IN REF. 2).
 SQ SEQUENCE 378 AA; 41239 MW; 58479E8685B43ED1 CRC64;

Query Match 78.8%; Score 1539.5; DB 1; Length 378;
 Best Local Similarity 77.3%; Pred. No. 7.1e-100;
 Matches 297; Conservative 24; Mismatches 40; Indels 23; Gaps 5;

QY 1 MRSKYLALLIPALLAAGAAHAAYYNNKDNKLDLYGKVDGLHYFSDNKCVDGDDQTYMRLG 60
 DB 1 MKAVYLSLLVPALLVAGANAAYEYNNKDNKLDLFGKYDGLHYFSDDGSGDDQTYMRLG 60
 QY 61 FKGETVTDLTGYGOWEYQIOGNSAENNNSWTRVAFAGLKFQDVSGSFYGRNYGVYD 120
 DB 61 FKGETVNDQLTGYGOWEYQIOGNTGEGSNDSWTRVAFAGLKFADAGSFYGRNYGVYD 120
 QY 121 VTSWTDVLPFEGGDTYGSNDNFMQORNGATYRTDFGLVDGLNFAVOYQKNGNSVGE 180
 DB 121 VTSWTDVLPFEGGDTYGSNDNFMQORNGATYRTDFGLVDGLNFAVOYQKNGNSVGE 180
 QY 181 GFTSGVTNNGRDALRONGDVGSGSTTYD-YEGFGIGAISSSKRTDAONTA---YING 236
 DB 181 -----NTNGSLNQNQDGGSGSTTYAIGGFSYSGAITTSKRRADONNTANRLYNG 234
 QY 237 DRAETTYGGLKYDANNIYLAQYTYTYNATRVG-----SLGMAKQNFENVAQYQ 287
 DB 235 DRAETTYGGLKYDANNIYLAQYQTYTYNATRVGSGNSPSTSGFANKQNFENVAQYQ 294
 QY 288 FDEGLRPSLALQSKGKRLGSG---YDDEDILKYVDYGAITYYFNKNMSTYVDKINLLD 343
 DB 295 FDFGLRPSVAALQSKGKRLGSGSGASVGDODIVRYVDGATYFENKNMSTYVDKINLLD 354
 QY 344 DNOFTRDAGINTDNIVALGLYQF 367
 DB 355 KNDFTRDAGINTDNIVALGLYQF 378

RESULT 3
 OMPC_KLEPN STANDARD; PRT; 363 AA.
 ID OMPC_KLEPN STANDARD; PRT; 363 AA.
 AC Q48473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC) (PORIN OMPC36).
 GN OMPC OR OMPC36.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=C3;
 RA MEDLINE=951172739; PubMed=7868262;
 RA Albert S., Rodriguez-Quiñones F., Schirmer T., Rummel G., Tomas J.M.,
 Rosenbusch J.P., Benedi V.J.;
 RT "A porin from Klebsiella pneumoniae: sequence homology, three-
 dimensional model, and complement binding.";
 RL Infect. Immun. 63:903-910(1995).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RX MEDLINE=99216538; PubMed=10196126;
 RA Dutzler R., Rummel G., Albert S., Hernandez-Alles S., Phale P.S.,
 Rosenbusch J.P., Benedi V.J., Schirmer T.;
 RT "Crystal structure and functional characterization of OmpK36, the
 RT osmoporin of Klebsiella pneumoniae.";
 RL Structure 7:425-434(1999).
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE. IN
 CC K. PNEUMONIAE IT HAS BEEN SHOWN TO BIND C1Q COMPONENT AND ACTIVATE
 CC THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/POE FAMILY OF PORINS.
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DR EMBL: Z33506; CA83913.1; -.
 DR PDB: 1OSW; 26-JUL-99.
 DR InterPro: IPR001702; -.
 DR InterPro: IPR001897; -.
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLIPORIN.
 DR PRINTS: PR00183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Transmembrane; Porin; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 363 OUTER MEMBRANE PROTEIN C.
 SQ SEQUENCE 363 AA; 39663 MW; 9DE45546F01F116C CRC64;

Query Match 78.7%; Score 1537; DB 1; Length 363;
 Best Local Similarity 78.9%; Pred. No. 1e-99;
 Matches 291; Conservative 32; Mismatches 38; Indels 8; Gaps 5;

QY 1 MRSKYLALLIPALLAAGAAHAAYYNNKDNKLDLYGKVDGLHYFSDNKCVDGDDQTYMRLG 60
 DB 1 MKAVYLSLLVPALLVAGANAAYEYNNKDNKLDLKGKIDGLHYFSDDGDDQTYMRLG 60
 QY 61 FKGETVTDLTGYGOWEYQIOGNSAENNN-SWTRVAFAGLKFQDVSGSFYGRNYGVY 119
 DB 61 VKGETQINDQLTGYGOWEYQIOGNSAENNN-SWTRVAFAGLKFQDVSGSFYGRNYGVY 120
 QY 120 DVTSTVDLPFEGGDTYGSNDNFMQORNGATYRTDFGLVDGLNFAVOYQKNGNSVSG 179
 DB 121 DVTSTVDLPFEGGDTYGSNDNFMQORNGATYRTDFGLVDGLNFAVOYQKNGNSVSG 180
 QY 180 EFTSGVTNNGRDALRONGDVGSGSTTYD-YEGFGIGAISSSKRTDAONTAAYTGNDR 238
 DB 181 E-----GATNNGRGALKQNGDVGSGSTTYDYGISAGFAVANSKRTDQDN-QLLGEGDH 235
 QY 239 AETTYGGLKYDANNIYLAQYTYTYNATRVGSLGANAQNFENVAQYQFDFGLRPSVAY 298
 DB 236 AETTYGGLKYDANNIYLAQYTYTYNATRVGSLGANAQNFENVAQYQFDFGLRPSVAY 295
 QY 299 LQSKGKRLGSGASVGDODIVRYVDGATYFENKNMSTYVDKINLLDNOFTRDAGINTDNI 358
 DB 296 LQSKGKRL-NGYGDQDLKYVDGATYFENKNMSTYVDKINLLDNOFTRDAGINTDNI 354
 QY 359 VALGLYQF 367
 DB 355 VALGLYQF 363

RESULT 4
 OMPC_SALTY STANDARD; PRT; 378 AA.
 ID OMPC_SALTY STANDARD; PRT; 378 AA.

OY 346 Q-FTRDAGINTDNIYALGVYQF 367
 1 :||||:||||:||||
 Db 361 DPEFKDAGISTDIDVALGVYQF 383

RESULT 6
OMP_N_ECOLI

OMP_N_ECOLI STANDARD; PRT; 377 AA.
 ID OMPN_ECOLI P76854;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE OUTER MEMBRANE PROTEIN N PRECURSOR (PORIN OMEN).
 GN OMPN.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-97251357; PubMed-9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sempel G., Seki Y., Sivasubaram S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horikuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE FROM N.A., SEQUENCE OF 22-33, AND CHARACTERIZATION.
 RX MEDLINE-98317278; PubMed-9642192;
 RA Prilipov A., Phale P.S., Koehnlik R., Widmer C., Rosenbusch J.P.;
 RT "Identification and characterization of two quiescent porin genes,
 ompC and ompN, in Escherichia coli BE.";
 RL J. Bacteriol. 180:3388-3392(1998).
 CC -1- FUNCTION: NON-SPECIFIC PORIN.
 CC -1- SUBUNIT: HOMOMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
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 CC EMBL: AE000234; AAC74459.1; -
 CC EMBL: D90775; BAA14981.1; -
 CC EMBL: D90776; BAA14986.1; -
 CC EcoGene: EG13375; OMPN.
 CC InterPro: IPR001702; -
 CC InterPro: IPR001897; -
 CC Pfam: PF00267; Gram-ve_porins; 1.
 CC PRINTS: PR00187; ECOLNIPORIN.
 CC PRINTS: PR00183; ECOLIPORIN.
 CC Outer membrane; transmembrane; Porin; Signal.
 FT SIGNAL 1 21

FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;

Query Match 66.3%; Score 1295; DB 1; Length 377;
 Best Local Similarity 67.8%; Pred. No. 6, 1e-83;
 Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

OY 1 MKSKVIALLPALLAAGAAHAEVYNDGKRLDLYGVDSGLHFSFNDKVDGQTYRLG 60
 |||||||
 Db 1 MKSKVIALLPALLAAGAAHAEVYNDGKRLDLYGVDSGLHFSFNDKVDGQTYRLG 60
 OY 61 FKGETOVTDLTGYGOWEYOIGNSAE--NENSWTRVAAGLKFQDVSFDRNGVYV 119
 |||||||
 Db 61 FKGETOINDLTGYGOWEYNOANTESSKNSQWTRLAFLKFAVDYSPDRNGVYV 120
 OY 120 DVTSMTDVLPEFGDPTV--GSDNEMQORNGATRYRNTDFGLVDGNTFAVOYQKGNPS 178
 |||||||
 Db 121 DIEGWTDMLEPEFGDSTYNADNMTGRANGVATRYRNTDFGLVNGLNFAYOYQGN-- 176
 OY 179 GEGFTSGV--TNGRDALRONGDVGGSITVDY--EGFGIGALISSKRTDAQ--NTPAYI 233
 ||:::|
 Db 177 -EGASNGQEGTNNGRDVRHENGWGSLSTYDGLMGFSAGAAATSSDRINDQVNHATA-- 233
 OY 234 GNCDRRETYTGKLYDANNITYLAQTYQYNAFVSLGW--ANKAQNFEAVAYQFDFG 291
 ||:::|
 Db 234 -GCDKADAMTAGLKDYDANNITYLATMYSETRNMTPEFGSDVAVANKTQNEFVTAQYQFDFG 292
 OY 292 LRPSLAVYLOSKGNL-----GRGYDEDILKYDVGYATYFNKMSYVDYKINLTD 343
 ||:::|
 Db 293 LRPAVSFLMSKGRDLHAAGADNPAGVDKLVKADYDGYATYFNKMSYVDYKINLTD 352
 OY 344 -DNQFTRDAGINTDNIYALGVYQF 367
 ||:::|
 Db 353 EDDSFYANGISTDIDVALGVYQF 377
 RESULT 7
 OMP_C_SERMA
 ID OMP_C_SERMA STANDARD; PRT; 376 AA.
 AC 054471;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMC).
 GN OMC.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UOC-51;
 RX MEDLINE-94236242; PubMed-8190703;
 RA Hutsl J.A.M., Worobec E.A.;
 RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
 marcescens.";
 RL Microbiology 140:379-387(1994).
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
 CC -1- SUBUNIT: HOMOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: I24960; AAA26562.1; -

DR InterPro: IPR001702; -
 DR InterPro: IPR001897; -
 DR Pfam: PF00267; Gram-ve.porins; 1.
 DR PRINTS: PR00182; ECOLIIPORIN.
 DR PRINTS: PR00183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 DR Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 1 22 OUTER MEMBRANE PROTEIN C.
 FT SEQUENCE 376 AA; 41440 MW; 81227FE8515B568E CRC64;

Query Match 65.7%; Score 1283.5; DB 1; Length 376;
 Best Local Similarity 65.6%; Pred. No. 3.8e-82;
 Matches 252; Conservative 48; Mismatches 59; Indels 25; Gaps 8;

QY 1 MKSKVALLPALLAAGAAHAAYVYKDKGKLDLYCKVDGLHFSNDKVDGDTYMRIG 60
 DB 1 MKLRVSLWVLPALLVAGTAGAAEYVYKDKGKLDLYCKVDGLHFSNNGVDSGYMRFG 60
 QY 61 FKGEVOTDQLTGYGMEYVQIGNSAENENN-SWTRVAFAGLFPDGVSPDYGRNYGVY 119
 DB 61 LREFTQISDQLTGYGMEYVQIGNSAENENN-SWTRVAFAGLFPDGVSPDYGRNYGVY 120
 QY 120 DVTSTWTDVLPFEGGDTYGSDFNFMOQRNGFATYRNTDFGLVDGLNFAVOYGRKNGNP 179
 DB 121 DVAAVTDLPFEGGDTYGSDFNFMOQRNGFATYRNTDFGLVDGLNFAVOYGRKNGNP 178
 QY 180 EGTSTVYNNGRALNRONGVGSGSTTYDEGFGI--GGAISSKRTDAONTA----AT 233
 DB 179 E-----ETNNGRVYLNQNGEGYSGMSYDM-GYISAGAFENSRSENGANGHONTM 232
 QY 234 GNDRAETVYGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAVAOY 288
 DB 233 GRDDKAEVSGGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAVAOY 288
 QY 289 DEGLRSLAYLQSKGNL--YDDEDLKYVDGATYVYENKMSYVYDKINLTD 343
 DB 293 DFLRFVGVYNTKQKDLGRAGNGKDYGDQDLVKEFVDLGFATYFFNKMSTYVYDKINLTD 352
 QY 344 DNOFTRDAGINTNTIYALGLYOF 367
 DB 353 NNDFTDAGINTNVAVGLYOF 376

RESULT 8
 OMPF_SERMA STANDARD; PRT; 374 AA.
 AC 03380;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).
 GN OMPF.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OOC-51;
 RX MEDLINE=97419518; PubMed=9274033;
 RA Hutul J.A.M., Morobec E.A.;
 RT "Molecular characterization of the Serratia marcescens OmpF porin,
 and analysis of S. marcescens OmpF and OmpC osmoregulation.";
 RL Microbiology 143:2797-2806(1997).
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMPF/PHOE FAMILY OF PORINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: U81967; AAB69103.1; ALT_INIT.
 DR InterPro: IPR001702; -
 DR InterPro: IPR001897; -
 DR Pfam: PF00267; Gram-ve.porins; 1.
 DR PRINTS: PR00182; ECOLIIPORIN.
 DR PRINTS: PR00183; ECOLIIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 DR Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 1 22 OUTER MEMBRANE PROTEIN F.
 FT SEQUENCE 374 AA; 41184 MW; BF821D385E441049 CRC64;

Query Match 63.5%; Score 1241; DB 1; Length 374;
 Best Local Similarity 64.3%; Pred. No. 3.3e-79;
 Matches 249; Conservative 36; Mismatches 68; Indels 34; Gaps 8;

QY 1 MKSKVALLPALLAAGAAHAAYVYKDKGKLDLYCKVDGLHFSNDKVDGDTYMRIG 60
 DB 2 MKRNIILAVVLPALLAAGAAHAAYVYKDKGKLDLYCKVDGLHFSNDKVDGDTYMRIG 61
 QY 61 FKGEVOTDQLTGYGMEYVQIGNSAENENN-SWTRVAFAGLFPDGVSPDYGRNYGVY 118
 DB 62 FKGEVOTDQLTGYGMEYVQIGNSAENENN-SWTRVAFAGLFPDGVSPDYGRNYGVY 121
 QY 119 YDVTSTWTDVLPFEGGDTYGSDFNFMOQRNGFATYRNTDFGLVDGLNFAVOYGRKNGNP 177
 DB 122 YDVGWTDVLPFEGGDTYGSDFNFMOQRNGFATYRNTDFGLVDGLNFAVOYGRKNGNP 178
 QY 178 SCGEFTSVYNNGRALNRONGVGSGSTTYDEGFGI--GGAISSKRTDAONTAATYICNG 236
 DB 179 -----QNDGRVYKQNGDGMGJISSTYDIGEYVFGAAYVASSNRTDOKLRSN-ERG 228
 QY 237 DRAETVYGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAV 283
 DB 229 DKRADNTVGAKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAV 288
 QY 284 AOYQFDEGLRPSLAYLQSKGNL--GRGYDDEDLKYVDGATYVYENKMSYVYDKIN 340
 DB 289 AOYQFDEGLRPSLAYLQSKGNLNPVGVG-SDDQLVKYVSGTYVYENKMSYVYDKIN 347
 QY 341 LDDNFTRDAGINTNTIYALGLYOF 367
 DB 348 LDDNFTRDAGINTNTIYALGLYOF 374

RESULT 9
 OMPF_RAHQA STANDARD; PRT; 342 AA.
 AC 033507;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN C (PORIN OMPF) (FRAGMENT).
 GN OMPF.
 OS Rahmella aquatilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Rahmella.
 OX NCBI_TaxID=34038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CF3;
 RX MEDLINE=98132388; PubMed=9473046;
 RA Achouak W., Pages J.M., de Mot R., Molle G., Heulin T.;
 RT "A major outer membrane protein of Rahmella aquatilis functions as a
 RT porin and root adhesin.";
 RL J. Bacteriol. 180:909-913(1998).
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR


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RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97213358; PubMed-9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN
RT DNA Res. 3:379-392(1996).
RN
RP CONCEPTUAL TRANSLATION.
RA Rodd K.E.;
RL Unpublished observations (JUN-1998).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMP/POPE FAMILY OF PORINS.
-1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION, AN IN-FRAME STOP CODON
WAS READ OVER IN POSITION 162 AND TWO POTENTIAL FRAMESHIFTS WERE
CORRECTED.
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CC -----
CC
DR EMBL: AE000288; AAC75030.1; ALT_FRAME.
DR EMBL: AE000288; AAC75031.1; ALT_FRAME.
DR EMBL: AE000288; AAC75032.1; ALT_FRAME.
DR EMBL: D90835; BAA15791.1; ALT_FRAME.
DR EMBL: D90835; BAA15792.1; ALT_FRAME.
DR EMBL: D90835; BAA15793.1; ALT_FRAME.
DR EcoGene: EGI4042; yed5.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00183; ECOLIPORIN.
DR PRINTS: PR00183; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Hypothetical protein; Outer membrane; Transmembrane; Porin; Signal.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 397 POTENTIAL.
FT CHAIN 23 42981 MW; 9C5183E5432FE0F0 CRC64;
SQ SEQUENCE 397 AA; 42981 MW; 9C5183E5432FE0F0 CRC64;

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Query Match 60.8%; Score 1187; DB 1; Length 397;
Best Local Similarity 61.0%; Pred. No. 1.9e-75;
Matches 244; Conservative 41; Mismatches 79; Indels 36; Gaps 10;

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QY 1 MKKVALALPALAAGAAHAAYVKNCKDLVYGVGLHFPNDKVDGQGTWRIG 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MKRKVALMLPALVAGAAVAAYVKNCKDLVYGVGLHFPNDKVDGQGTWRIG 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 FKGETOVDTLNGYGMWEYVIOGNSAENE-NNSWTRVAFAGLKEFDVGSFGRRNGVY 119
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FKGETIADDTGYGMWEFNIGANGPESDKGNATRLAFLGFGNGTGYGRNGVY 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 120 DVTSMVDLVEFGGDYV-GSDNFMQQRNGNGATYRMTDFEGLVDGLNFAVQYQGRN-6N 176
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 DVAEMTDMLPEFGGDYVAGADNFMNNGRANGVATYRNNNGFGYVDGLNFAVQYQGRN-6N 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 PSG-EGFTSVYTNNGRDLRQNDGVGGSTTYDYE-GFGIGALISSKRRDAQ----- 227
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 PFGDEGSGSG---DGRLSKENDGFGMSTSYDPEFGLSLGAAYXNSDRDQVGYGLND 237
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 228 -NTAAATGNGDRAETVYTGKLYDANNITVLAQYQYNNATRVGS-----LGNANKA 277
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 238 RNHSNRNAGGETAEATVYTGKLYDANNITVLAQYQYNNATRVGS-----LGNANKA 297
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 278 QNEFAVAQYQFDEGLRSLATVYQSKGNLQ-----RGYDEEDILKVVYDGYATYFN 328
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 298 QNEFAVAQYQFDEGLRSLATVYQSKGNLQ-----RGYDEEDILKVVYDGYATYFN 357
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 329 KNNSTVYDKINILD-DNQTFRDAGINTDITVALGLVYQF 367
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 358 KNNSTVYDKINILD-DNQTFRDAGINTDITVALGLVYQF 397
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 12
NMPC_ECOLI STANDARD: PRT: 365 AA.
ID NMPC_ECOLI
AC P21420; P77189;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORIN PROTEIN NMPC PRECURSOR.
GN NMPC OR PHMA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MUTANT CS384;
RX MEDLINE-86304457; PubMed-3017988;
RA Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;
RT "Structure of the lc and nmcp outer membrane porin protein genes of
lambdaoid bacteriophage.";
RL J. Biol. Chem. 261:12723-12732(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JL5502;
RX MEDLINE-94355635; PubMed-8057841;
RA Coll J.B., Heyde M., Portallier R.;
RT "Expression of the nmcp gene of Escherichia coli K-12 is modulated by
external pH. Identification of cis-acting regulatory sequences
involved in this regulation.";
RL Mol. Microbiol. 12:83-93(1994).
RN [4]
RP SEQUENCE OF 347-365 FROM N.A.
RC STRAIN-K12;
RX MEDLINE-96196428; PubMed-8648624;
RA Mahdi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
RT "Holiday junction resolvases encoded by homologous rusa genes in

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RT Escherichia coli K-12 and phage 82.;

RL J. Mol. Biol. 257:561-573(1996).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.

CC MISCELLANEOUS: IN WILD-TYPE STRAINS OF E. COLI K12, THE NMPC OPEN

CC READING FRAME IS INTERRUPTED BY AN IS5 INSERTION AND GENERATES A

CC HYBRID OPEN READING FRAME THAT IS NOT EXPRESSED. HOWEVER, IN

CC MUTANT STRAIN CS348, THE IS5 ELEMENT HAS BEEN DELETED AND NMPC IS

CC EXPRESSED.

CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.

CC -----

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DR EMBL; M13457; AAA23728.1; ALT_SEQ.

DR EMBL; AE000160; AAC73654.1; ALT_SEQ.

DR EMBL; U82598; AAB40749.1; ALT_SEQ.

DR EMBL; Z35442; CAA84594.1; -.

DR EMBL; X32587; CAA63323.1; -.

DR PIR; A25647; MMECNC.

DR HSSP; P02931; IGFN.

DR EcoGene; EGI0659; nmPC.

DR InterPro; IPR001702; -.

DR InterPro; IPR001897; -.

DR Pfam; PF00267; Gram-ve_porins; 1.

DR PRINTS; PR00182; ECOLNEIPORIN.

DR PRINTS; PR00183; ECOLIPORIN.

DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.

KW Outer membrane; Transmembrane; Porin; Signal.

FT SIGNAL 1 23

FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN NMPC.

FT CONFLICT 326 326 K -> N (IN REF. 2 AND 3).

FT SEQUENCE 365 AA; 40316 MW; 6E5128D4847FB4F8 CRC64;

Query Match 60.3%; Score 1177; DB 1; Length 365;

Best Local Similarity 62.1%; Pred. No. 8.7e-75;

Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;

QY 1 MRSKVLAL--LIPALLAAGAAHAEEYNNKDKNLIDLYGKVDGLHYFSNDKNDVGDQTYMR 58

DB 1 MKKLITVAISVAASVLAAMSAQAALIEYNNKDSNKLIDLYGKNAHVFSSNDADGDTTYAR 60

QY 59 LGKGETOYTDLTGFGQWEYIOGNSAENENS--WTRVAFAGLKFQDYGSPDYGRNNG 116

DB 61 LGKGETOYTDLTGFGQWEYEFKGNRAESQSSKDKTRLAFAGLKEGYSIDYGRNNG 120

QY 117 VYVDVTSMTDVLPEFGGDY--GSDNFMQORGNFGATYRTNDFGLVDGLNFAVOYGRKNG 175

DB 121 VAYDIGAMTDVLPDEFGGDTWTQTDVMTQRTATVATYRNNDPFGLVGLNFAAOYGRKND 180

QY 176 NPSGEGFTSGVTNNRGDALRONGDVGSGSTTYDEGFGIGALSSSKRRDAONTAAYI-- 233

DB 181 RSPDNTES-----NKGDFGFSATYIEEGFGIGATYAKSDRDTDYNAGKVL 229

QY 234 ---GNGDRAETTYGGLKYDANNIYLAAYTQTYNATRVGSLGNKNAQNEAVALYOQDFE 290

DB 230 EYVASGKNAEVMAAGLKYDANNIYLAATYSETQNTVFADHFAVANKAQNFEAVALYOQDFE 289

QY 291 GLRPSLAYLOSCKNGRGVDEDDILKYVDGATYTFENKMSYTYVYKTNLLDDNQTRD 350

DB 290 GLRPSVAAYLOSCKRDLG--WGDODLVKYVDGATYTFENKMSYTYVYKTNLLDDNQTRD 348

QY 351 AGINTDINVALGLVYOF 367

DB 349 LGVSTDIVAVGLVYOF 365

RESULT 13

PORL.BPPA2

ID PORL.BPPA2 STANDARD; PRT; 365 AA.

AC P07238;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE OUTER MEMBRANE PORIN PROTEIN LC PRECURSOR.

GN LC.

OS Bacteriophage PA-2.

OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.

OX NCBI_Taxid=10738;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-86304457; PubMed-3017988;

RA Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;

RT "Structure of the lc and nmPC outer membrane porin protein genes of

RT lambdaoid bacteriophage".

RL J. Biol. Chem. 261:12723-12732(1986).

CC -1- FUNCTION: PORINS ARE MAJOR PROTEINS FOUND IN THE OUTER MEMBRANES

CC OF GRAM-NEGATIVE BACTERIA WHERE THEY FORM CHANNELS FOR THE

CC NONSPECIFIC PERMEATION OF SMALL SOLUTES (MOLECULES WITH MW LOWER

CC THAN 4000-6000 DALTONS).

CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE

CC (BY SIMILARITY).

CC -1- MISCELLANEOUS: A PORIN GENE CAN ALSO BE FOUND IN THE GENOMES OF

CC CERTAIN LAMBDOID BACTERIOPHAGE, AND ITS PROTEIN IS EXPRESSED IN

CC THE LYSOGENIC STATE. IN E. COLI THE EXPRESSION OF OMPC AND OMPF

CC PROTEINS IS THEN REDUCED SUBSTANTIALLY.

CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.

CC -----

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CC -----

DR EMBL; J02580; AAA2301.1; -.

DR PIR; D25647; MMBP2.

DR HSSP; P02931; IGFN.

DR InterPro; IPR001702; -.

DR InterPro; IPR001897; -.

DR Pfam; PF00267; Gram-ve_porins; 1.

DR PRINTS; PR00182; ECOLNEIPORIN.

DR PRINTS; PR00183; ECOLIPORIN.

DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.

KW Outer membrane; Transmembrane; Porin; Signal.

FT SIGNAL 1 23

FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN LC.

FT CONFLICT 99 99 H -> R (IN AA SEQUENCE).

FT SEQUENCE 365 AA; 40290 MW; 0FBC0531FB9C0205 CRC64;

Query Match 59.9%; Score 1169; DB 1; Length 365;

Best Local Similarity 61.8%; Pred. No. 3.1e-74;

Matches 233; Conservative 41; Mismatches 81; Indels 22; Gaps 6;

QY 1 MRSKVLAL--LIPALLAAGAAHAEEYNNKDKNLIDLYGKVDGLHYFSNDKNDVGDQTYMR 58

DB 1 MKKLITVAISVAASVLAAMSAQAALIEYNNKDSNKLIDLYGKNAHVFSSNDADGDTTYAR 60

QY 59 LGKGETOYTDLTGFGQWEYIOGNSAENENS--WTRVAFAGLKFQDYGSPDYGRNNG 116

DB 61 LGKGETOYTDLTGFGQWEYEFKGNRAESQSSKDKTRLAFAGLKEGYSIDYGRNNG 120

QY 117 VYVDVTSMTDVLPEFGGDY--GSDNFMQORGNFGATYRTNDFGLVDGLNFAVOYGRKNG 175

DB 121 VAYDIGAMTDVLPDEFGGDTWTQTDVMTQRTATVATYRNNDPFGLVGLNFAAOYGRKND 180

QY 176 NPSGEGFTSGVTNNRGDALRONGDVGSGSTTYDEGFGIGALSSSKRRDAONTAAYI-- 233

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=84297232; PubMed=6089111;
 RA Deutch A.H., Rushlow K.E., Smith C.J.;
 RT "Analysis of the Escherichia coli PROA locus by DNA and protein
 sequencing.";
 RL Nucleic Acids Res. 12:6337-6355(1984).
 RN [6]
 RP MUTAGENESIS OF PHE-351
 RX MEDLINE=91162638; PubMed=1848301;
 RA Struyve M., Moons M., Tommassen J.;
 RT "Carboxy-terminal phenylalanine is essential for the correct assembly
 of a bacterial outer membrane protein.";
 RL J. Mol. Biol. 218:141-148(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).
 RX MEDLINE=91172301; PubMed=1848682;
 RA Jap B.K., Walian P.J., Gehring K.;
 RT "Structural architecture of an outer membrane channel as determined
 by electron crystallography.";
 RL Nature 350:167-170(1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=92375189; PubMed=1380671;
 RA Cowan S.W., Schirmer T., Rummel G., Steiert M., Ghosh R.,
 RA Pauplit R.A., Jansonius J.N., Rosenbusch J.P.;
 RT "Crystal structures explain functional properties of two E. coli
 porins.";
 RL Nature 358:727-733(1992).
 RN [9]
 RP TOPOLOGY.
 RX MEDLINE=93172954; PubMed=7679770;
 RA Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;
 RT "Topology of Phob porin: the 'eyelet' region.";
 RL Mol. Microbiol. 7:131-140(1993).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN E. COLI CELLS
 ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
 PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
 PHOSPHORLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
 SOLUTES.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMP/C/POE FAMILY OF PORINS.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: V00316; CAA23605.1; -;
 DR EMBL: D83536; BAA77910.1; -;
 DR EMBL: AE000132; AAC73345.1; -;
 DR EMBL: U70214; AAB08661.1; -;
 DR EMBL: X00786; CAA25362.1; -;
 DR PIR: A03432; MMECEP.
 DR PDB: 1PHO; 3I-OCT-93.
 DR SWISS-2DPAGE: P02932; COLI.
 DR ECO2DBASE: B037.0; 6TH EDITION.
 DR EcGene: EG10729; POE.
 DR InterPro: IPR001702; -;
 DR InterPro: IPR001897; -;
 DR Pfam: PF00267; Gram-ve_porins; 1.
 DR PRINTS: PR00182; ECOLIPORIN.
 DR PRINTS: PR00183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Transmembrane; Porin; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 351
 FT MUTAGEN 351 351
 FT OUTER MEMBRANE PORE PROTEIN E.
 FT F->Y,N,S,V: LESS RESISTANT TO TRYPSIN.

FT STRAND 25 26
 FT STRAND 30 35
 FT STRAND 37 45
 FT STRAND 52 53
 FT STRAND 56 63
 FT STRAND 71 82
 FT TURN 87 88
 FT STRAND 93 104
 FT TURN 105 107
 FT STRAND 108 116
 FT TURN 119 119
 FT HELIX 120 123
 FT TURN 124 126
 FT TURN 140 141
 FT TURN 143 145
 FT STRAND 147 157
 FT TURN 159 162
 FT TURN 164 165
 FT STRAND 166 173
 FT STRAND 176 176
 FT TURN 182 183
 FT STRAND 185 185
 FT STRAND 188 197
 FT TURN 198 201
 FT STRAND 202 212
 FT HELIX 215 217
 FT TURN 218 219
 FT STRAND 227 239
 FT TURN 240 241
 FT STRAND 242 252
 FT STRAND 264 274
 FT STRAND 280 292
 FT STRAND 294 294
 FT TURN 295 297
 FT STRAND 298 298
 FT STRAND 301 313
 FT STRAND 318 327
 FT TURN 334 335
 FT STRAND 342 350
 SQ SEQUENCE 351 AA; 38922 MR; 249E2E362C030C9A CRC64;
 Query Match 56.8%; Score 1109; DB 1; Length 351;
 Best Local Similarity 58.3%; Pred. No. 4.3e-70;
 Matches 217; Conservative 53; Mismatches 76; Indels 26; Gaps 9;
 QY 1 MKSVYLLALIPALLAAGAAHAAYVYKNDGKLDLYGKVDGLHYSDNKNVDGDDOTYARLG 60
 DB 1 MKSVYLLALIPALLAAGAAHAAYVYKNDGKLDLYGKVDGLHYSDNKNVDGDDOTYARLG 60
 QY 61 FKGETOYTDOLTYGOWEYOLOGNSAENEN-NSWTRVAFAGLKRQDYSPDYGKNGYVY 119
 DB 61 FKGETOYTDOLTYGOWEYOLOGNSAENEN-NSWTRVAFAGLKRQDYSPDYGKNGYVY 119
 QY 120 DVTSMYDVLPEFGSDTYG-SDNFMOQRNGFATYRNTDFGLVDGLNFAVOYQKNGNPS 178
 DB 120 DVTSMYDVLPEFGSDTYG-SDNFMOQRNGFATYRNTDFGLVDGLNFAVOYQKNGNPS 178
 QY 121 DVEAMTDMFPEFGSDSSAQTDNFMFKRASGLATYRNTDFGLVDGLNFAVOYQKNGNPS 178
 DB 121 DVEAMTDMFPEFGSDSSAQTDNFMFKRASGLATYRNTDFGLVDGLNFAVOYQKNGNPS 178
 QY 179 GEGFTSGVTNNGDALRONGDVGGSITYDEG--FGIGCAISSSKRTDAQNTAAYIGNG 236
 DB 179 GEGFTSGVTNNGDALRONGDVGGSITYDEG--FGIGCAISSSKRTDAQNTAAYIGNG 236
 QY 179 -----RDVKRQNGDGFSTSLYDFGSGDFAISGAYVTRSDRTEQNLOS-R-GTG 225
 DB 179 -----RDVKRQNGDGFSTSLYDFGSGDFAISGAYVTRSDRTEQNLOS-R-GTG 225
 QY 237 DRAETTYGGLKYDANNNTYLAQYQTYNATRVVSLGMANKRQNEAVAOYQDFGLRPSL 296
 DB 237 DRAETTYGGLKYDANNNTYLAQYQTYNATRVVSLGMANKRQNEAVAOYQDFGLRPSL 296
 QY 226 KRAEAMATGLKYDANNNTYLAQYQTYNATRVVSLGMANKRQNEAVAOYQDFGLRPSL 284
 DB 226 KRAEAMATGLKYDANNNTYLAQYQTYNATRVVSLGMANKRQNEAVAOYQDFGLRPSL 284
 QY 297 AYLOSCKNLGRGYDDEDLKYVDVGVATYFENKMSYVYDKILDL-DNQFTPDAGINT 355
 DB 297 AYLOSCKNLGRGYDDEDLKYVDVGVATYFENKMSYVYDKILDL-DNQFTPDAGINT 355
 QY 285 GYVLSKSKDI-EGIGDEDLVYIDVGATYFENKMSAFVYDKINQDSDKL-----NINN 339
 DB 285 GYVLSKSKDI-EGIGDEDLVYIDVGATYFENKMSAFVYDKINQDSDKL-----NINN 339
 QY 356 DNIVAGLVYQF 367
 DB 356 DNIVAGLVYQF 367
 QY 340 DDIYAVGMFYQF 351
 DB 340 DDIYAVGMFYQF 351

Tue Aug 21 21:40:18 2001

us-09-575-061-1.rsp

Page 12

Search completed: August 21, 2001, 20:59:41
Job time: 116 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 15.97 Seconds
(Without alignments)
1750.536 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 1953
Sequence: 1 MRSKVALIPALLAGAAH.....TRDAGINTNIVALGLVYQF 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	1 MMECP	outer membrane por
2	1804	92.4	367	2 B85861	outer membrane por
3	1539.5	78.8	378	1 MMEBPC	outer membrane por
4	1537	78.7	363	2 S51104	outer membrane por
5	1512.5	77.4	378	1 A59139	outer membrane por
6	1295	66.3	377	2 D64888	outer membrane por
7	1213.5	62.1	394	2 S34263	outer membrane por
8	1177	60.3	365	1 MMECNC	outer membrane por
9	1174	60.1	365	1 MMEBPC	outer membrane por
10	1142.5	58.5	366	2 B85729	probable outer mem
11	1109	56.8	351	1 MMEBPC	outer membrane por
12	1109	56.8	351	2 B85113	outer membrane por
13	1104	56.5	362	1 MMECF	outer membrane por
14	1104	56.5	362	2 B85619	outer membrane por
15	1086	55.6	351	2 S25520	outer membrane por
16	1065.5	54.6	350	2 S23525	outer membrane por
17	1055.5	54.0	350	2 S36606	outer membrane por
18	1027.5	52.6	363	2 S43159	outer membrane por
19	1002	51.3	369	2 S70847	outer membrane por
20	733.5	37.6	255	2 D85740	partial probable o
21	732	37.5	315	2 T46993	hypothetical prote
22	692	35.4	224	2 F85814	probable outer mem
23	600	30.7	171	2 B64960	outer membrane por
24	592	30.3	382	2 G84971	ompF-like porin (l
25	522.5	26.8	123	2 C85740	partial probable o
26	478	24.5	191	2 G85814	probable outer mem
27	388.5	19.9	134	2 B64961	outer membrane por
28	310	15.9	96	2 C64900	outer membrane por
29	279	14.3	350	2 A82299	outer membrane pro

30	254	13.0	331	2 E82389	probable outer mem
31	215.5	11.0	97	2 A57983	outer membrane por
32	194.5	10.0	371	2 S68072	major outer membra
33	194.5	10.0	371	2 S68069	major outer membra
34	176	9.0	386	2 S68062	major outer membra
35	174.5	8.9	326	2 JN0792	porin-like protein
36	173.5	8.9	385	2 S68066	major outer membra
37	172.5	8.8	385	2 S68067	major outer membra
38	169.5	8.7	385	2 S68070	major outer membra
39	169	8.7	50	2 T46990	hypothetical prote
40	168.5	8.6	351	2 JC6314	major porin protei
41	165	8.4	330	2 PC4425	lectin-like adhesi
42	164.5	8.4	361	2 A30542	major outer membra
43	163.5	8.4	359	2 D64050	major outer membra
44	156.5	8.0	368	2 A82148	probable porin VC1
45	155	7.9	360	2 S17456	outer membrane pro

ALIGNMENTS

RESULT 1
MMECP
Outer membrane porin ompC precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #extl_change 16-Jul-1999
C:Accession: A20867; A18885; B25029; E64991
R:Mizuno, T.; Chou, M.Y.; Inouye, M.
J. Biol. Chem. 258, 6932-6940, 1983
A:Title: A comparative study on the genes for three porins of the Escherichia coli ou
A:Reference number: A20867; MUID:83213433
A:Accession: A20867
A:Molecule type: DNA
A:Residues: 1-367 <MID>
A:Cross-references: GB:K00541; GB:M10314; GB:M14188; NID:g147007; PIDN:AAA24243.1; PI
R:Mizuno, T.; Chou, M.Y.; Inouye, M.
FEBS Lett. 151, 159-164, 1983
A:Title: DNA sequence of the promoter region of the ompC gene and the amino acid sequ
A:Reference number: A18885; MUID:83132326
A:Accession: A18885
A:Molecule type: DNA
A:Residues: 1-40 <MID>
R:Nogami, T.; Mizuno, T.; Mizushima, S.
J. Bacteriol. 164, 797-801, 1985
A:Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous r
A:Reference number: A91809; MUID:86033642
A:Accession: B25029
A:Molecule type: DNA
A:Residues: 32-57 <NOG>
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: E64991
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <BLAT>
A:Cross-references: GB:AE000310; GB:U00096; NID:g2367131; PIDN:AACT5275.1; PID:g17885
A:Experimental source: strain K-12, substrain MG1655
A:Gene: ompC
A:Map position: 47 min
C:Function:
A:Description: one of the E. coli major outer membrane proteins that form passive dif
C:Superfamily: outer membrane protein porF
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-367/Product: outer membrane porin ompC #status predicted <MAT>

Query Match 98.0%; Score 1914; DB 1; Length 367;
Best Local Similarity 98.1%; Pred. No. 5,6e-127;

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Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MRSKVALALIPALLAAGAAHAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
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Db 1 MKKRVSLILVALLVAGAAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
QY 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
QY 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
QY 181 GFTSGVTNNGRDALRONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 240
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 GFTSGVTNNGRDALRONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 240
QY 241 TYTGGLKYDANNIYLAAYQTQYNATRVGSLGWANKAQNFEAAVAYQFDFGLRPSLAYLQ 300
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TYTGGLKYDANNIYLAAYQTQYNATRVGSLGWANKAQNFEAAVAYQFDFGLRPSLAYLQ 300
QY 301 SKRKNLGRGDDDDILKYVDVGAATYFNKMSYVDKINLLDDNQPTRAGINTDNIYA 360
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SKRKNLGRGDDDDILKYVDVGAATYFNKMSYVDKINLLDDNQPTRAGINTDNIYA 360
QY 361 LGLVYQF 367
  |||:|||||
Db 361 LGLVYQF 367

RESULT 2
B85861
outer membrane protein 1b (Ibc) [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B85861
R:Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
  Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
  Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <STO>
A:Cross-references: GB:AE005174; NID:g12516550; PIDN:AA657350.1; GSPDB:GN00145; UNGP:234
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ompC
C:Superfamily: outer membrane protein phoE
```

```
Query Match 92.4%; Score 1804; DB 2; Length 367;
Best Local Similarity 92.5%; Pred. No. 2.9e-119;
Matches 343; Conservative 9; Mismatches 11; Indels 8; Gaps 2;
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```
QY 1 MRSKVALALIPALLAAGAAHAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
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Db 1 MKKRVSLILVALLVAGAAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
QY 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
QY 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
QY 181 GFTSGVTNNGRDALRONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 240
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 -----GFTSGVTNNGRDALRONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 236
```

```
QY 241 TYTGGLKYDANNIYLAAYQTQYNATRVGSLGWANKAQNFEAAVAYQFDFGLRPSLAYLQ 300
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 TYTGGLKYDANNIYLAAYQTQYNATRVGSLGWANKAQNFEAAVAYQFDFGLRPSLAYLQ 296
QY 301 SKRKNL-----GRGDDDDILKYVDVGAATYFNKMSYVDKINLLDDNQPTRAGINTD 356
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 SKRKNLGVINGRNVDDDDILKYVDVGAATYFNKMSYVDKINLLDDNQPTRAGINTD 356
QY 357 NIVALGLVYQF 367
  |||:|||||
Db 357 NIVALGLVYQF 367
```

```
RESULT 3
MMEBPC
outer membrane porin ompC precursor - Salmonella typhi
C:Species: Salmonella typhi
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: J00119; S01248; S10122
R:Puentes, J.L.; Alvarez-Scherer, V.; Gosset, G.; Calva, E.
  Gene 83, 197-206, 1989
A:Title: Comparative analysis of the Salmonella typhi and Escherichia coli ompC genes
A:Reference number: J00119; MUID:90060831
A:Accession: J00119
A:Molecule type: DNA
A:Residues: 1-378 <PUE>
A:Cross-references: GB:M31424; NID:g154207; PIDN:AA27169.1; PID:g154208
R:Venegas, A.; Gomez, I.; Zaror, I.; Yudelevich, A.
  Nucleic Acids Res. 16, 7721, 1988
A:Title: The nucleotide sequence of the Salmonella typhi ompC porin gene.
A:Reference number: S01248; MUID:88319959
A:Accession: S01248
A:Molecule type: DNA
A:Residues: 1-5, 'Q', 7-361, 363-378 <VEN1>
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797
A:Experimental source: strain Ty2
R:Venegas, A.
  submitted to the EMBL Data Library, May 1988
A:Reference number: S10122
A:Accession: S10122
A:Molecule type: DNA
A:Residues: 1-361, 363-378 <VEN2>
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797
C:Genetics:
A:Gene: ompC
A:Map position: 45 min
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-378/Product: outer membrane porin ompC #status predicted <MAT>
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Query Match 78.8%; Score 1539.5; DB 1; Length 378;
Best Local Similarity 77.3%; Pred. No. 1e-100;
Matches 297; Conservative 24; Mismatches 40; Indels 23; Gaps 5;
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```
QY 1 MRSKVALALIPALLAAGAAHAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKKRVSLILVALLVAGAAAEVYNNKDKNKLDLYGKVDGLHYFSDNKKVDGDOTYMRIG 60
QY 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FKEGTQVTDLTGCGWMEYOIQGNSAENENNSWTRVAFAGLKFQDVGSFDPYGRNYGVYD 120
QY 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VTSMTDVLPEFGGDTYGSNFMQGRNGFATYNTDPEFGLVLDLNFVAYOGKNGNSPGE 180
QY 181 GFTSGVTNNGRDALRONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 236
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 -----NTNKRSLNONGDVGSGITYDYEGFISGALISSSKRTDAQNTAAVYIGNGRAE 234
QY 237 DRAEYTGGLKYDANNIYLAAYQTQYNATRVG-----SLGWANKAQNFEAAVAYQF 287
```

Accession	Sequence	Position
Dd	235 DRATVYTGGLAYDANNIYLLAAQYSGTVAATNPFGLSNGSNGSNSTSGFANKNAQNEFVAQAQY	294
Qy	268 FDFGIRPSBLATLQSKKKKLGRC---YDDEDILKYYVDVGYATYFNKMKMSTYVDIKINLLD	343
Dd	295 FDFGIRPSVAALQSKGKISNGYSGASYGDODIVKYVDVGATYTYFNKMKMSTYVDYKINLLD	354
Qy	344 DNOFTRDAGINTDNIVALLGLVYQF 367	
Dd	355 KNDFTKRGAGINTDIDIVALGLVYQF 378	

```

RESULT      4
S51104
outer membrane porin ompK36 precursor - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C:Accession: S51104
R:Alberti, S.
submitted to the EMBL Data Library, May 1994
A:Description: A porin from Klebsiella pneumoniae: sequence homology, three-dimensional
A:Reference number: S51104
A:Accession: S51104
A:Molecule type: DNA
A:Residues: 1-363 <ALB>
A:Cross-references: EMBL:Z3506; NID:g2104843; PIDN:CAA639J.1; PID:g619891
C:Genetics:
A:Gene: ompK36
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-363/Product: outer membrane porin ompK36 #status predicted <MAT>

```

Query Match	78.7%	Score 1537	DB 2	Length 365
Best Local Similarity	78.9%	Pred. No. 1.5e+100		
Matches 291	Conservative 32	Mismatches 38	Indels 8	Gaps 5

QY	1	MKSRYIALLLIPALLAAGAAHAEYNNKDNKLDYGVVDGLJHFSDNKDYVDGQOTYRILG	60
Dd	1	MKVAVLSLVLVALLVAGANAAEITYNNKDNKLDLYGKIDGJLHFSDDKVDVGQOTYRILG	60
QY	61	EKGETOVTDLQTLGYGOWEYOIOGNSAENENN-SWTRAFAAGLKFQDYGSGFDYGRNIGVYV	119
Dd	61	VKGEGTQINDQTLGYGOWEYVNNQANNTESSSDQANTRLATFAGLKRKGADSGSFDYGRNIGVYV	120
QY	120	DYTSWTDYLVPEFGGDIYGSDFPMQQRNFEGATYRNTDFEGLVDCGLNFAYVYQCKNGNPSG	179
Dd	121	DYTSWTDYLVPEFGGDIYGSDFLPSRANGVATYRNSDFEGLVDCGLNFALYOCKNGNSVSG	180
QY	180	EGFTSGYVNNRQDLNRONGDSVGSITYYD-YEGRGIGLAISSSKRMDQNTAAYIGNGDR	238
Dd	181	E-----GATNNRKGALKONGDSEFTSVYTDLPDGISAGFAVANSKRITDDQN-QLLLEGGDH	235
QY	239	AETTYGGLKDYDANNIYYAAOQTYQTYNNATRYGSLGMNAKKAQNFEEVAQYQDFGLRPSLAY	298
Dd	236	AETTYGGLKDYDANNIYYATQTYQTYNNATRYGSLGCFPAKKAQNFEEVAQYQDFGLRPSVAY	295
QY	299	LQSGKGNLGRGCTDEDEDILKTYVDGATYYFNNKMSYVDYKINLLDNOQFTRDAGINTDNI	358
Dd	296	LQSGKGNLGRGCTDEDEDILKTYVDGATYYFNNKMSYVDYKINLLDNRFTSRAGISITDNDV	354
QY	359	VALGLVYQF 367	
Dd	355	VALGLVYQF 363	

RESULT 5
A59139
outer membrane porin C precursor - *Salmonella typhimurium*
N:Alternate names: ompC protein
C:Species: *Salmonella typhimurium*
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999

C:Accession: A59139
R:Negm, R.S.: Pistole, T.G.
Can. J. Microbiol. 45, 658-669, 1999
A>Title: The porin OmpC of *Salmonella typhimurium* mediates adherence to macrophages
A:Reference number: A59139; MUID:99457705
A:Accession: A59139
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-378 <NEG>
A:Cross-References: GB:AF039309; NID:g2773086; PIDN:AAB96675.1; PID:g2773087
A:Experimental source: strain 14028
A:Note: submitted to Genbank, December 1997
C:Genetics:
A:Gene: ompC
A:Map position: 49.3 minutes
C:Complex: homotrimer
C:Superfamily: outer membrane protein phoE
C:Keywords: homotrimer; membrane protein; porin
F:1-31/Domain: signal sequence #status predicted <Sig>
F:22-378/Product: outer membrane porin ompC #status predicted <MAT>

Query Match	Similarity	77.4%	Score 1512.5	DB 1	Length 378
Best Local	Similarity	76.6%	Pred. No. 8e-99		
Matches	294	Conservative	26	Mismatches	41
				Indels	23
				Gaps	6
Qy	1	MKSKVLLALLPALLAAGAAAEVYNNKDGKLDLYCKYDGLHYFSDNKNKDVGDQTYMRIG	60		
Db	1	MKVKVLSTLPLPALLVAGAAANAAEIVYNNKDGKLDLFGKYDGLHYFSDDKSGSDQTYMRIG	60		
Qy	61	FKGEIYQVMDQLGYGQWQEWQIQGNSAENNNNSWTVAFGLKFEQVQSGSPDYRANRYGYVD	120		
Db	61	FKGEIYQVMDQLGYGQWQEWQIQGNOTEGSSNDSWTRAFGLKFPALGSDPYRANRYGYVD	120		
Qy	121	VYSWTDVLPPEFGDGYGSDNFMQQRGNFQATYRNTDFFELVYDGLNFAVYQYQKNGNPSGE	180		
Db	121	VYSWTDVLPPEFGDGYGADNFMQQRGNFQATYRNTDFFELVYDGLNFAVYQYQKNGNPSGE	180		
Qy	181	GFTSGVTNNGRDALNQNGDVGSGSTTYDY-EEFGIGAGISSKRT-DAONT--AAVINGG	236		
Db	181	-----NTMGSRSLNQNGDVGSGSTLYAAGEFVSAGATTSKRTADODPNTANARLYGNG	234		
Qy	237	DRAETTYGGLKTDANNIYLAAYQTYTVAATRYG-----SLGMAKNAQNEPVAAYQY	287		
Db	235	DRAIYTYGGLKTDANNIYLAAYQTYTVAATRYGTSNGSNPSTSYGFANKAQNEPVAAYQY	294		
Qy	288	FDFGGLRPSLAVYQSGKGNILGRG-----YDDEDLIKYVDVAGATYTFPKNMSTYVDYKINILD	343		
Db	295	FDFGGLRPSLAVYQSGKGNILGRG-----YDDEDLIKYVDVAGATYTFPKNMSTYVDYKINILD	354		
Qy	344	DNQFTRDAGINTDNIVAGLVYQF	367		
Db	355	KYEFTRDAGINTDNIVAGLVYQF	378		

RESULT 6
D64888
outer membrane porin bl377 precursor - *Escherichia coli*
C:Species: *Escherichia coli*
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C:Accession: D64888
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: D64888
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-377 <BLAT>
A:Cross-references: GB:AE000234; GB:U00096; NID:g187633; PIDN:AAC74459.1; PID:g1876
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: outer membrane protein phob

C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <Sig>
F:22-37/Product: probable outer membrane porin b1377 #status predicted <Opp>

Query Match 66.3%; Score 1295; DB 2; Length 377;

Best Local Similarity 67.8%; Pred. No. 1.4e-83;

Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

```

QY 1 MKSKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFPDNKKVDGQDTYRRLG 60
    |||||||
DB 1 MKSKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFPDNKKVDGQDTYRRLG 60
    |||||||
QY 61 FKKEITVDTDLTGCGMEYIOGNSAEN-NNNSMTRAVAFGLFODGSPDYGRNNGVY 119
    |||||||
DB 61 FKKEITVDTDLTGCGMEYIOGNSAEN-NNNSMTRAVAFGLFODGSPDYGRNNGVY 119
    |||||||
QY 120 DVTSWTDVLPFEGGDTY-GSDNFMQGRNGFATYRNTDFGLVDGLFAVOYOGKNGNPS 178
    |||||||
DB 121 DIGMTDMLPEFGGDSYTNADNEMTGANGVATYRNTDFGLVDGLFAVOYOGKNGNPS 176
    |||||||
QY 179 GEFTSGV--TNNGRDLRNGDVGSGITYDY-EGFGIGALISSKRTDAQ--NTAAIT 233
    |||||
DB 177 -EGASNGQECTNGRDVRRHENGSGWGLSTYDLMGMSAAGAAATSSDRTDQVNHNTAA-- 233
    |||||
QY 234 GNGDRAETTYGGLKYDANNITYLAQYTOTYNTATRVGSLGW--ANKAQNFPFAVAVOYOFDFG 291
    |||||
DB 234 -GGDKKADWATAGLKYDANNITYLATMYSETRNMTPEFGSDSYAVANKTONFEVTAQYOFDFG 292
    |||||
QY 292 LRPSLAYLOSQRNL-----GRGYDEDLIKYVDGATYFNNKMSYVDYKINLMD 343
    |||||
DB 293 LRPAVSFLMSKGRDLNHAAGADNPAGVDKDLVKADIGATYFNNKMSYVDYKINLMD 352
    |||||
QY 344 -DNQFTRDAGINTDNTVALGLVYQF 367
    |||||
DB 353 EDDSFYAANGISTYDVALGLVYQF 377
    |||||

```

RESULT 7

S34263

outer membrane porin ompF precursor - Salmonella typhi

C:Species: Salmonella typhi

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S34263

R.Fernandez-Mora, M.; Calva, E.

Submitted to the EMBL Data Library, June 1993

A:Reference number: S34263

A:Accession: S34263

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <FER>

A:Cross-references: EMBL:K7327; NID:g602362; PIDN:CAA51710.1; PID:g311957

C:Genetics:

A:Gene: ompF

C:Superfamily: outer membrane protein phoe

C:Keywords: membrane protein; porin; trimer

F:1-21/Domain: signal sequence #status predicted <Sig>

F:22-394/Product: outer membrane porin ompF #status predicted <Mat>

Query Match 62.1%; Score 1213.5; DB 2; Length 394;

Best Local Similarity 62.8%; Pred. No. 7.5e-78;

Matches 248; Conservative 38; Mismatches 80; Indels 29; Gaps 10;

```

QY 1 MKSKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFPDNKKVDGQDTYRRLG 60
    |||||||
DB 1 MNKKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFPDNKKVDGQDTYRRLG 60
    |||||||
QY 61 FKKEITVDTDLTGCGMEYIOGNSAEN-NSMTRAVAFGLFODGSPDYGRNNGVY 119
    |||||||
DB 61 FKKEITVDTDLTGCGMEYIOGNSAEN-NSMTRAVAFGLFODGSPDYGRNNGVY 119
    |||||||
QY 120 DVTSWTDVLPFEGGDTY-GSDNFMQGRNGFATYRNTDFGLVDGLFAVOYOGKNGNPS 178
    |||||||

```

```

DB 121 DIAMWTDALPEFGGDTYQTDVYMLGRTNGVATYRNTDFEGLVGLFAVOYOGKNGNEN-G 179
    |||||||
QY 179 GEFTSGVTNNG-RDLRNGDVGSGITYDY-EGFGIGALISSKRTDAQNTAAI----- 232
    |||||||
DB 180 GAGAGDGTGNGNRKLARENGDGFSGMSTSYDFPGLSLGAAYSSDSRSDQVARGDGM 239
    |||||||
QY 233 -----TGNGRATETTYGGLKYDANNITYLAQYTOTYNTATRV-----GSLGMANKAQNFE 281
    |||||||
DB 240 NERNNNAAGETALAWITGAKYDANVYLAAMVAFETRNMTYGGGNGEKGNSINKTONFE 299
    |||||||
QY 282 AVAQYOFDFGLRPSLAYLOSQRNLG-----RG---YDEDLIKYVDGATYFNNKMS 333
    |||||||
DB 300 VVAQYOFDFGLRPSLAYLOSQRNLGEGVEYHRGMRMTDILVKYVDGATYFNNKMS 359
    |||||||
QY 334 YVDYKINLMD-DNQFTRDAGINTDNTVALGLVYQF 367
    |||||||
DB 360 YVDYKINLMDDEDDFYANNIGATIDTIVGLVYQF 394
    |||||||

```

RESULT 8

MNECNC

outer membrane porin mmpC precursor - Escherichia coli cryptic lambdoid prophage DLP1

C:Species: Escherichia coli

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999

C:Accession: A25647; S66594; G64787

R.Blaabrand, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A.

J. Biol. Chem. 261, 12723-12732, 1986

A:Title: Structure of the Ic and mmpC outer membrane porin protein genes of lambdoid

A:Reference number: A25647; MUID:86304457

A:Contents: mutant strain CS384

A:Accession: A25647

A:Molecule type: DNA

A:Residues: 1-365 <BLA>

R.Mandl, A.A.; Sharples, G.J.; Mandel, T.N.; Lloyd, R.G.

J. Mol. Biol. 257, 561-573, 1996

A:Title: Holliday junction resolvases encoded by homologous rusa genes in Escherichia

A:Reference number: S66579; MUID:96196428

A:Accession: S66594

A:Molecule type: DNA

A:Residues: 347-365 <MAN>

A:Cross-references: EMBL:X92587; NID:g1051136; PIDN:CAA63325.1; PID:g1051145

R.Blaabrand, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: G64787

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 'MNTRYAVTSFNNSSKRLT', 1-325, 'N', 327-347, 'EGANKSLI' <BLAT>

A:Cross-references: GB:AE000160; GB:U00096; NID:g1786751; PIDN:AAC73654.1; PID:g17867

A:Experimental source: strain K-12, substrain MG1655

C:Comment: In wild-type strains of E. coli K-12, the mmpC open reading frame is inter

ain CS348, the IS5 element has been deleted and mmpC is expressed.

C:Genetics:

A:Gene: mmpC

A:Map position: 12 min

A:Genome: cryptic lambdoid prophage DLP12

C:Superfamily: outer membrane protein phoe

C:Keywords: membrane protein; porin; trimer

F:1-23/Domain: signal sequence #status predicted <Sig>

F:24-365/Product: outer membrane porin mmpC #status predicted <Mat>

Query Match 60.3%; Score 1177; DB 1; Length 365;

Best Local Similarity 62.1%; Pred. No. 2.5e-75;

Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;

```

QY 1 MKSKVAL--LIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFPDNKKVDGQDTYR 58
    |||||
DB 1 MKKLTVAISVAASVLAASQAABEITNKDSNKLIDYGVNAKHFFSSNDADDGDTTAR 60
    |||||

```


[illegible]

QY 1 MKSLALLLLPALLAAGAAHAAEYVNRKGNKLDLYGKYDGLHYPSDNKDNDGDDQTYRBLG 60
Db 1 MKLIVAVVYVGLLAANVAHAAEYVNRKGNKLDLYGKYLALRYFTDDKRDGDDKTYARLG 60
QY 61 FKGETQVVDLTGTGOWEYQIQG--NSAENNNNSWTRAFAGLKFQDYGSPFDYGRNYGV 118
Db 61 FKGETQIWDQWIGGCHWMEYDFPKGYNDENANGSRDNKTRALAYAGLKISEGSLIDYGRNYGV 120
QY 119 YDVTSWTDVLPPEFGDFYVG-SDNFMQGRNGNFGATYRNTDFPGLVDGLNFAVOYGKGNP 177
Db 121 YDISWTDMLPEFGDPMQSKDVFMTYRTGVATYRANDFGLLEGLNFAVOYGKGNR- 179
QY 178 SGGEFTSGCVTNN---GRDALRQNGDVGSGITTYDESGFSGIGAISSSKRTDAQNTAA-- 231
Db 180 -----FDNSHLYGADYTRANGDGFGISSTYYDGFSGICAVYTKSDRNTAORAAAN 230
QY 232 -YIENGDRAEYFTYGLKRYKDANNITLLAAQYQTYNATRGSIGMANKNKNQNEFAVAQYORDF 290
Db 231 PLNAGSGNAELMAGIKIKDANNITFAANYAETLNNMTTYGDAYISNKAKSPFVAQYORDF 290
QY 291 GLRPSLAYLOSKGNKRLGCHYDEDEILKIVDYGATYVFNKNNSTYVDYITINLLDNOQFTR 350
Db 291 GLRPSLAYLKSKGIDLGR-YGDQDMIEIYDYGATYFFPKNNSTYVDYKINLIDESDFTRA 349
QY 351 AGINTDNIVALGLYQF 367
Db 350 VDIRTNIVATGYTQF 366

RESULT 11
MMECPE
outer membrane porin phoE precursor - Escherichia coli
C/Species: Escherichia coli
C/Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C/Accession: A03432; B64749
R:/Overbeek, N.; Bergmans, H.; van Mansfeld, F.; Lugtenberg, B.
J. Mol. Biol. 163, 513-532, 1983
A/Title: Complete nucleotide sequence of phoE, the structural gene for the phosphate
A/Reference number: A92893; WUID:83189086
A/Accession: A03432

A:Molecule type: protein
 A:Residues: 23-87, 'E', 89-138, 'G', 140-283, 'L', 285-362 <CHP>
 R:Nogami, T.; Mizuno, T.; Mizushima, S.
 J. Bacteriol. 164, 797-801, 1985
 A>Title: Construction of a series of ompF-ompC chimeric genes by in vivo homologous recombination
 A:Reference number: A91809; MID:86033642
 A:Accession: A25029
 A:Molecule type: DNA
 A:Residues: 33-63 <NOG>
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MID:97426617
 A:Accession: H64832
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Gene: ompF; tofF; cmfB; coa; cry
 A:Map position: 21 min
 C:Complex: homotrimer
 C:Function: <POR>
 A:Description: forms aqueous channels that facilitate diffusion of small hydrophilic molecules
 C:Function: <REC>
 A:Superfamily: receptor for bacteriophage T2
 C:Keywords: outer membrane protein phoE
 F:1-22/Domain: signal sequence #status predicted <Sig>
 F:23-362/Product: outer membrane protein ompF #status experimental <Mat>

Query Match 56.5%; Score 1104; DB 1; Length 362;
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

```

1  MKSKVLLALIPALLAAGAAHAEEYNNKDKNKLDPYGVKGLHYFS-----DNKDVDDQF 55
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2  MKRIILAVIYPALLVAGTANAAETYNKDKGNKVDLYGKAVGLHFSKNGENSGNGDMT 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 YMRIGFGETQVTDOLTGYGQWEYQIOGNSAEN---ENNSWTRVAFAGLRFODVGSFDYG 112
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 YARLGEFGETQINSDLTGYGQWEYNEFGNNSGADQGTGKTRLAFLAGLYADVGSFDYG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 RNYGVYDVTSMTDYLPEFGGDTYGSNPMQQRNGFATRNDFGLVGLFAVQYOG 172
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 RNYGVYDALGYTDMLEPFEGGDTAYSDDFVGRGVATYRNSNFFGLVGLNFAVQYLG 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 KNGNPSGEFTSGVTNNGRD-ALRONGDYGSGITTYDEFGIGAGATSSSKRTDAONTAA 231
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 K-----NERTPARNSGDVGSGSYTEBEGFVGAGADRNMLDE-AQ 225
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
232 YIGNGDAETTYTGLKYDANNIYLAAYOTQYNTATRV-----GSLGANKRQNEFAVAY 286
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
226 PLNGKKAQEWMAWGLKYDANNIYLAANYGETRATPTTNKFTNSGFRANKTQDVLVAQY 285
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 QPFEGFLRPSLAITYQSKGNKRGYDDEDILKYDVCAITYFNKRMSTYVYKINLDD-DN 345
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
286 QPFEGFLRPSLAITYKRSKAKDV-EGIGVDVLYNFEVGATYFNKRMSTYVYIINQIDSDN 344
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 QFTRDAGINTDNIVALGLVQYOF 367
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
345 KL-----GVGSDDTVAAGVITYOF 362
  
```

RESULT 14
 B85619
 Outer membrane protein 1a (1a,b,f) [imported] - *Escherichia coli* (strain O157:H7)
 C:Species: *Escherichia coli*
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: B83619

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A85480; MID:21074935; PMID:11206551
 A:Accession: B85619
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-362 <STO>
 A:Cross-references: GB:AE005174; NID:912514104; PIDN:AAG55414.1; GSPDB:GN00145; UMGF:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ompF
 C:Superfamily: outer membrane protein phoE

Query Match 56.5%; Score 1104; DB 2; Length 362;
 Best Local Similarity 58.9%; Pred. No. 3.2e-70;
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

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1  MKSKVLLALIPALLAAGAAHAEEYNNKDKNKLDPYGVKGLHYFS-----DNKDVDDQF 55
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2  MKRIILAVIYPALLVAGTANAAETYNKDKGNKVDLYGKAVGLHFSKNGENSGNGDMT 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 YMRIGFGETQVTDOLTGYGQWEYQIOGNSAEN---ENNSWTRVAFAGLRFODVGSFDYG 112
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 YARLGEFGETQINSDLTGYGQWEYNEFGNNSGADQGTGKTRLAFLAGLYADVGSFDYG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 RNYGVYDVTSMTDYLPEFGGDTYGSNPMQQRNGFATRNDFGLVGLFAVQYOG 172
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 RNYGVYDALGYTDMLEPFEGGDTAYSDDFVGRGVATYRNSNFFGLVGLNFAVQYLG 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 KNGNPSGEFTSGVTNNGRD-ALRONGDYGSGITTYDEFGIGAGATSSSKRTDAONTAA 231
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 K-----NERTPARNSGDVGSGSYTEBEGFVGAGADRNMLDE-AQ 225
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
232 YIGNGDAETTYTGLKYDANNIYLAAYOTQYNTATRVGS-----LGWANKRQNEFAVAY 286
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
226 ILGNGKKAQEWMAWGLKYDANNIYLAANYGETRATPTTNKFTNSGFRANKTQDVLVAQY 285
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 QPFEGFLRPSLAITYQSKGNKRGYDDEDILKYDVCAITYFNKRMSTYVYKINLDD-DN 345
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
286 QPFEGFLRPSLAITYKRSKAKDV-EGIGVDVLYNFEVGATYFNKRMSTYVYIINQIDSDN 344
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 QFTRDAGINTDNIVALGLVQYOF 367
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345 KL-----GVGSDDTVAAGVITYOF 362
  
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RESULT 15
 S25520
 Outer membrane protein phoE precursor - *Citrobacter freundii*
 C:Species: *Citrobacter freundii*
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
 C:Accession: S25520
 R:Pierings, G.; Ockhuysen, C.; Hofstra, H.; Tommassen, J.
 submitted to the EMBL Data Library, August 1992
 A:Reference number: S25520
 A:Accession: S25520
 A:Molecule type: DNA
 A:Residues: 1-351 <SPI>
 A:Cross-references: EMBL:X68021; NID:940474; PIDN:CAA48162.1; PID:940475
 A:Note: this is one of the proteins induced when the *E. coli* cells are grown under ph
 d compounds, and some other negatively charged solutes
 C:Genetics:
 A:Gene: phoE
 C:Complex: homotrimer
 C:Function:
 A:Description: allows passive diffusion of small hydrophilic molecules with molecular
 A:Note: induced under phosphate limitation
 C:Superfamily: outer membrane protein phoE
 C:Keywords: homotrimer; membrane protein; porin
 F:1-21/Domain: signal sequence #status predicted <Sig>

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 12.35 Seconds

(without alignments)
611.875 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953

Sequence: 1 MKSKVLAALLPALLAAGAAH.....TRDAGINTNIVALGLVYQF 367

Scoring table: BIOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Dackfilest1.pep:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	US-09-041-889-30	Sequence 30, Appl
2	1285	65.8	377	US-09-041-889-29	Sequence 29, Appl
3	1078.5	55.2	323	US-09-041-889-28	Sequence 28, Appl
4	1027	52.6	340	US-08-355-844-1	Sequence 1, Appl
5	1027	52.6	340	PCT-US95-16126-1	Sequence 1, Appl
6	164.5	8.4	361	US-08-096-181A-8	Sequence 8, Appl
7	164.5	8.4	361	PCT-US94-08326-8	Sequence 8, Appl
8	140.5	7.2	342	US-08-096-182A-4	Sequence 4, Appl
9	140.5	7.2	342	US-08-877-109-4	Sequence 4, Appl
10	140.5	7.2	342	US-08-798-760-4	Sequence 4, Appl
11	140.5	7.2	342	PCT-US94-08327-4	Sequence 4, Appl
12	140.5	7.2	363	US-08-096-182A-6	Sequence 6, Appl
13	140.5	7.2	363	US-08-877-109-6	Sequence 6, Appl
14	140.5	7.2	363	US-08-798-760-6	Sequence 6, Appl
15	140.5	7.2	363	PCT-US94-08327-6	Sequence 6, Appl
16	128.5	6.6	589	US-09-377-155-19	Sequence 19, Appl
17	127.5	6.5	363	US-08-096-181A-10	Sequence 10, Appl
18	127.5	6.5	363	PCT-US94-08326-10	Sequence 10, Appl
19	126.5	6.5	342	US-08-096-181A-12	Sequence 12, Appl
20	126.5	6.5	342	US-08-096-181A-14	Sequence 14, Appl
21	126.5	6.5	342	PCT-US94-08326-14	Sequence 14, Appl
22	124.5	6.4	511	US-08-480-604A-20	Sequence 20, Appl
23	124.5	6.4	511	US-08-405-496A-20	Sequence 20, Appl
24	124.5	6.4	608	US-08-480-604A-21	Sequence 21, Appl
25	124.5	6.4	608	US-08-405-496A-21	Sequence 21, Appl
26	124.5	6.4	609	US-08-480-604A-30	Sequence 30, Appl

28	124.5	6.4	2366	1	US-08-480-604A-10	Sequence 10, Appl
29	124.5	6.4	2366	2	US-08-405-496A-10	Sequence 10, Appl
30	118.5	6.1	309	1	US-08-096-182A-2	Sequence 2, Appl
31	118.5	6.1	309	1	US-08-877-109-2	Sequence 2, Appl
32	118.5	6.1	309	3	US-08-798-760-2	Sequence 2, Appl
33	118.5	6.1	309	5	PCT-US94-08327-2	Sequence 2, Appl
34	116.5	5.8	598	4	US-09-377-155-5	Sequence 5, Appl
35	116.5	5.8	592	4	US-09-377-155-17	Sequence 17, Appl
36	113.5	5.8	594	4	US-09-377-155-15	Sequence 15, Appl
37	112.5	5.8	594	4	US-09-377-155-7	Sequence 7, Appl
38	112.5	5.8	1657	3	US-09-057-570-2	Sequence 2, Appl
39	112.5	5.8	1805	3	US-09-057-570-7	Sequence 7, Appl
40	111.5	5.7	398	4	US-09-377-155-13	Sequence 13, Appl
41	111	5.7	3031	1	US-07-689-008-2	Sequence 2, Appl
42	110.5	5.7	591	4	US-09-377-155-11	Sequence 11, Appl
43	110.5	5.7	591	4	US-09-377-155-21	Sequence 21, Appl
44	110.5	5.7	592	4	US-09-377-155-2	Sequence 2, Appl
45	110	5.6	341	2	US-08-538-711A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-041-889-30
; Sequence 30, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; ATTORNEY: Conavy, Olier
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PW 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9601
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-889-30

Query Match 98.0%; Score 1914; DB 3; Length 367;
Best Local Similarity 98.1%; Pred. No. 1,4e-157;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKYKVLILVLPALLVAGAAHAEVYNNKDLGYKVDGLHYFSDNKKVDGDQTYMRIG 60
QY 61 FKGETVOTDQLTGYGQMEVYIOGNSAENENNSWTRAFALFKQDVGSFPGYGRNYYVD 120
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FKGETVOTDQLTGYGQMEVYIOGNSAENENNSWTRAFALFKQDVGSFPGYGRNYYVD 120
QY 121 VTSMTDVLPEFGGDTYGSDFMOGRNFEGATYRNTDFEGLVDGLNFAVOYQGNKNGPSGE 180
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Db 121 VTSMTDVLPEFGGDTYGSDFMOGRNFEGATYRNTDFEGLVDGLNFAVOYQGNKNGPSGE 180
QY 181 GFPSGYTNGRDALRONGDVGSGITYDEFGSIGAIISSSKRTDAONTAAYIGNGDRAE 240
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 GFPSGYTNGRDALRONGDVGSGITYDEFGSIGAIISSSKRTDAONTAAYIGNGDRAE 240
QY 241 TYTGSLKYDANNITYLAOYQOTNATRVGSLGNANKAONEAVALQOFDGLRPSLAYIQ 300
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TYTGSLKYDANNITYLAOYQOTNATRVGSLGNANKAONEAVALQOFDGLRPSLAYIQ 300
QY 301 SKGKNLGRGYDDEDLKYVDVGATYFNKMSYVDYKINLDDNOFTRDAGINTDNIYA 360
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Db 301 SKGKNLGRGYDDEDLKYVDVGATYFNKMSYVDYKINLDDNOFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
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Db 361 LGLVYQF 367
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RESULT 2

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US-09-041-889-29
; Sequence 29, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-889-29
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Query Match 65.8%; Score 1285; DB 3; Length 377;
Best Local Similarity 67.3%; Pred. No. 2,8e-103;
Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;

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Db 1 MRSKVALLIPALLAAGAAHAEVYNNKDGKLDLYGKVDGLHYFSDNKKVDGDQTYMRIG 60
QY 61 FKGETVOTDQLTGYGQMEVYIOGNSAE-MENNSWTRAFALFKQDVGSFPGYGRNYYVD 119
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FKGETVOTDQLTGYGQMEVYIOGNSAE--MNNSTWTRAFALFKQDVGSFPGYGRNYYVD 120
QY 120 DVTSMTDVLPEFGGDTY--GSDNFMQGRNFEGATYRNTDFEGLVDGLNFAVOYQGNKNGPS 178
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DIEGWTDLMLPEFGGDTYNTADNFMTRANGVATYRNTDFEGLVNGLNFAVOYQGN-- 176
QY 179 GEGFTSGV--TNGRDALRONGDVGSGITYDY--EFGSIGAIISSSKRTDAQ--NTAAYI 233
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 -EGASNGQEGTNGRDVRRHENGDMGLSTTYDLGMGFSAGAATSSDRINDQVNHATA-- 233
QY 234 GNGDRAETTTGGLKYDANNITYLAOYQOTNATRVGSLGM--ANKAONEAVALQOFDGE 291
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Db 234 -GGDKADAMTAGLKYPDANNITYLATMYSETRNMTPEGSDPYAAVANKTQNEVTAQOFDEG 292
QY 292 LRPSLAYLOSCKNL-----GRGYDDEDLKYVDVGATYFNKMSYVDYKINLDD 343
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Db 293 LRPAVSFLMSKGRDLHAAGADNPAGVDDKDLKYKADIGATYFNKMSYVDYKINLDD 352
QY 344 -DNQFTRDAGINTDNIYALGLVYQF 367
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Db 353 EDDSFYAANGISPDIDVALGLVYQF 377
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RESULT 3

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US-09-041-889-28
; Sequence 28, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 28:
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SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-041-889-28

Query Match 55.2%; Score 1078.5; DB 3; Length 323;
 Best Local Similarity 66.2%; Pred. No. 1.5e-85;
 Matches 219; Conservative 31; Mismatches 36; Indels 25; Gaps 9;

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 1 MMSKVLALLIPALAAAGAAAEVYNNKDKNKLIDYGVGLHYFSDNKNVDVDDQTYRMIG 60
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 61 FKGFTQVVDLTGCGMEYQIOGNSAE--NENSWTRVAFAGLKFDQVGSFDYGRNYGVY 119
 61 FKGFTQVVDLTGCGMEYQIOGNSAE--NENSWTRVAFAGLKFDQVGSFDYGRNYGVY 119
 120 DVTSMVDLPERGSDTY--GSDNFMQORGNFGATYRNTDPEFGLVDGLNFAVOYQGNKGPS 178
 121 DIEGFTDMIPERGSDSYTNADNFMTRNGAVATYRNTDPEFGLVNGLNFAVOYQGNK---- 176
 179 GEGFTSGV--TNNGRDALRONGDVGSGITYDY--EGFGTGAISSSKRTDAQ--NTAAVI 233
 177 -EGASNGEGFTNGRDVHEHNGDGLSTYDGLGKFSAGAAVTSDDRTNQVNHATA-- 233
 234 GNGDAEFTYTGKTDANNITLAAYITOTYNATRVGSLGW--ANKAQNFEAVAOYQDFPG 291
 234 -GGDAADMTAGLKYDANNIYATATYSETRNMTPEGSDSYAVANKTONFEVYAGYQDFPG 292
 292 LRPSLAVLOSCKGNL-----GRGYDDED 314
 293 LRPAVSFLMSKGRDLHAAGADNPAGVDDKD 323

RESULT 4
 US-08-355-844-1

Sequence 1, Application US/08355844
 Patent No. 5940307
 GENERAL INFORMATION:
 APPLICANT: Fischbarg, Jorge
 APPLICANT: Czegledy, Ferenc
 APPLICANT: Iserovich, Pavel
 APPLICANT: Li, Jun
 APPLICANT: Cheung, Min
 TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
 TITLE OF INVENTION: STRUCTURE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10112-0228
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/355,844
 FILING DATE: 14-DEC-1994
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Tang, Henry Y.S.
 REGISTRATION NUMBER: 29,705
 REFERENCE/DOCKET NUMBER: A29927-50/29910
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-408-2586
 TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 340 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Escherichia coli
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..340
 OTHER INFORMATION: OmpF porin protein
 US-08-355-844-1

Query Match 52.6%; Score 1027; DB 2; Length 340;
 Best Local Similarity 58.4%; Pred. No. 4.5e-81;
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

22 AEVYNNKDKNKLIDYGVGLHYFSDNKNVDVDDQTYRMIG 76
 1 AEVYNNKDKNKLIDYGVGLHYFSDNKNVDVDDQTYRMIG 76
 77 WEYQIOGNSAE--NENSWTRVAFAGLKFDQVGSFDYGRNYGVYDVTSMVDLPERG 133
 61 WEYNNQGNSEADADQNTKTRLAFLAGLKADVGSFDYGRNYGVYDGLGTDMLPERG 120
 134 DTGSDNFMQORGNFGATYRNTDPEFGLVDGLNFAVOYQGNKNGSGEFTSGVTNNGD- 192
 121 DTAVSDDFEVRGVGAVATYRNSNFEGLVDGLNFAVOYLGK-----NERDT 165
 193 ALRONGDVGSGITYDYRNGFGTGAISSSKRTDAQNTAAVYNGDRATYNGLKTDANN 252
 166 ARSNGDVGSGISTEYBFGIVGAYGADRINLDE--AQLGNGKAKAOMATGLKTDANN 224
 253 IYLAAYTQTYNATRV-----GSLGMANKAQNFEAVAOYQDFGLRPSLAVLOSCKGNIG 307
 225 IYLAAYTQTYNATRV-----GSLGMANKAQNFEAVAOYQDFGLRPSLAVLOSCKGNIG 283
 308 RGYDDEDILKTYVDGATYRNNKSTVYKINLID--DNOFTRDAGINTDVALGLVYQ 366
 284 EGIGVDVLYNFEVAGATYRNNKSTVYKINLID--DNOFTRDAGINTDVALGLVYQ 339
 367 F 367
 340 F 340

RESULT 5
 PCT-US95-16126-1

Sequence 1, Application PC/WTUS9516126
 GENERAL INFORMATION:
 APPLICANT: Fischbarg, Jorge
 APPLICANT: Czegledy, Ferenc
 APPLICANT: Iserovich, Pavel
 APPLICANT: Li, Jun
 APPLICANT: Cheung, Min
 TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
 TITLE OF INVENTION: STRUCTURE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10112-0228
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,844
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A29927-50/29910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..340
OTHER INFORMATION: OmpF porin protein
PCT-US95-16126-1
```

```

Query Match      52.6%; Score 1027; DB 5; Length 340;
Best Local Similarity 58.4%; Pred. No. 4.5e-81;
Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;
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```

QY 22 AEVYKNGKRLDLYGKVDGLHYF-----DNKDVDSQDTYKRLGKGETQVTDLTGCG 76
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 AEIYKNGKRLDLYGKVDGLHYF-----DNKDVDSQDTYKRLGKGETQVTDLTGCG 60
QY 77 WEYIOGSAEN--ENNSMTRVAFAGLKPDVGSFDYGRNYGVVYVTSATDVLPERGG 133
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 61 WEYFQGNNSGADAGQGNKTRLAFLAGLKADVGSFDYGRNYGVVYVTSATDVLPERGG 120
QY 134 DTVSGDFMOQRNGFATYRTDFFGLVDGLNFAVYQGNKNGSGEGFTSGVYNNGRD- 192
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 121 DTVASDDEFVRGVGATVYRNSNFFGLVDGLNFAVYQGNKNGSGEGFTSGVYNNGRD- 165
QY 193 ALRNGGCVGSGTYDEDEGIGAISSSKRTDQNTAATYIGNDRRAETITGKRYANN 252
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 166 ARRSNGGCVGSGTYDEDEGIGAISSSKRTDQNTAATYIGNDRRAETITGKRYANN 224
QY 253 IYLAQYTOTYNATRV-----GSLGMANKAQNFEAVAQYQDFGLRPSLAYLQSKGKRLG 307
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 225 IYLAANYGERNNATPIINKTFTNTSGFANKQDVLVAQYQDFGLRPSLAYLQSKGKRLG 283
QY 308 RGYDDEDILKIVDYGATYFNKNKSTYVDYKINILD-DNQFTRDAGINTNTVALGLVYQ 366
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 284 EGIQDVLVNVFEVYGATYFNKNKSTYVDYKINILD-DNQFTRDAGINTNTVALGLVYQ 339
QY 367 F 367
DB 340 F 340
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```

RESULT 6
US-08-096-181A-8
; Sequence 8, Application US/08096181A
; Patent No. 6153406
; GENERAL INFORMATION:
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Pullen, Jeffrey K.
; APPLICANT: Soper, Thomas S.
; APPLICANT: Liang, Shu-Mei
; TITLE OF INVENTION: A Method For The High Level Expression,
```

```

TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane Protein
TITLE OF INVENTION: P2 From Haemophilus Influenzae Type b
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,181A
FILING DATE: 23-Jul-1993
CLASSIFICATION: 424
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-181A-8
```

```

Query Match      8.4%; Score 164.5; DB 4; Length 361;
Best Local Similarity 24.1%; Pred. No. 1.4e-06;
Matches 90; Conservative 52; Mismatches 145; Indels 87; Gaps 17;
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```

QY 4 KYALLIPALLAAGAAHAEEVYKNGKRLDLYGKVDGLHYFSDNKVDGDTY----- 56
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3 KTLAALIVGAFASAAANAAYVYNNEGTNVELGRLSTIAEQS-NSTVDNKKOQHGLRLNG 61
QY 57 -MRIGFGEFOVTDLTGCGMEYQIOGNSAENNSM-----TRVAFAGLKPDVGSFDY 111
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 62 GSRFHIAKTHNFGDGYAQGYLTFRYTKASGSDNFGDITSKYAVYVLTGNATFEVKL 121
QY 112 GRNGVYVDTWMTDVPFEGCDTYGSDNFMQGRN-FGATYRNTDFFGLVDGLNFAVYQ 170
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 122 GRKTIADGITSAD--KEYG--VLNNSDYIPTSGNTVGTFRGID--GLVLGANT----- 171
QY 171 QGNKNGSGEGFTSGVYNNGRDALRONGDVGSGITYDYEGFIGAISSSKRTDQNTA 230
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 172 -----LLAQKREGAKG-----ENKRPNDKAGE 193
QY 231 AVIG---NGDRAETTYGSLYDANNITYLAQYTOT---YNATRVGSLGMANKAO--NFEA 282
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 194 VRIGELNNGIQV-----GAKYDANDIYAKIATYGRITNKYHESD-----EHKQQLNGVLA 242
QY 283 VAOYQF-DFLRPSLAYLQSKGKRLGSGYDDEDILKIVDYGATYFNKNKSTYVDYKI-- 339
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 243 TLGYRFSDLGLVSLDSGVAKTKNYKLIKHEKR--YFVSGFQYELMEDTINVGKRFYER 299
QY 340 NLDDNQFTRDAGI 353
DB 300 TSVDOGEKTRDOAV 313
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RESULT 7
PCT-US94-08326-8
; Sequence 8, Application PC/TUS9408326
; GENERAL INFORMATION:
; APPLICANT: North American Vaccine, Inc.
; APPLICANT: 12103 Indian Creek Court
; APPLICANT: Beltsville, MD 20705
; APPLICANT: Pullen, Jeffrey K.
; APPLICANT: Soper, Thomas S.
```



```

APPLICANT: Liang, Shu-Mei
TITLE OF INVENTION: A Method For The High Level
TITLE OF INVENTION: Expression,
TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane
TITLE OF INVENTION: Protein
TITLE OF INVENTION: P2 From Haemophilus Influenzae Type b
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08326
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,181
FILING DATE: 23-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REFERENCE/DOCKET NUMBER: 1438.001PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08326-8

```

```

Query Match      8.48; Score 164.5; DB 5; Length 361;
Best Local Similarity 24.18; Pred. No. 1.4e-06;
Matches 90; Conservative 52; Mismatches 145; Indels 87; Gaps 17;

QY 4 KVLALLPALLAAGAAAEVYNDGKLDLYGKVDLHFFSDKRDVDSQTY----- 56
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3 KITLALLVGAFAASAAAYNNNEGTVNELGRLIILAEOS-NSTVDNOKOCHGALRNQ 61
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 57 -MRIGFGEYQVTDQLTGYGOWEYQIOGNSAENENNSW---TRVAFAGLKFQDVGSEFDY 111
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 62 GSRFHKATHNFGDGYAQCGLFTRFVTKASENGSDNFGDITTSKYAVVTLGNKAFGEVKL 121
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 112 GRNGVYVDTSMVDLPEFGDGYGSDNFMQOGRN-FGATYRNTDFPGLVDGLNFAVQY 170
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 122 GRATYADGITSAD--KEVG--VLNNSDYIPIPSGNTGYTFKCID--GVLGANY---- 171
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 171 QGKNGNSGEGFTSGYTNNGRDALRONGDVGSGITVDYEGFGLGALISSKRRDAQNTA 230
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 172 -----LAAQRREGAKG-----ENKRRNDKAGE 193
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 231 AYIG--NGRAETYTGLKYDANNIYLAQYTOT--YNATRVGSLGMANKAQ--NFEA 282
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 194 VRIGEINNNGIYV-----GAKYDANDIVAKIAYGRNTYKNYESD-----EKKQQLNVLVA 242
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 283 VAQYQF-DGFLRPSLATLQSKGKGLGSGYDDEDLIKLYVDVGAITYFNKNNSTYVDYKI-- 339
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 243 TLGFRFSDGLGLVSLDQSGYAKTKNYKIKHEKR--YFVSPGFQYELMEDTNYVGNFYER 299
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 340 NLDDNOFTRDAGI 353
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 300 TSVDOGKRETRQAV 313
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 8
US-08-096-182A-4
; Sequence 4, Application US/08096182A
; Patent No. 5439808
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Hulin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
; TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,182A
; FILING DATE: 23-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-096-182A-4

```

```

Query Match      7.28; Score 140.5; DB 1; Length 342;
Best Local Similarity 25.68; Pred. No. 0.00015;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RIGFKEGYQVTDQLTGYGOWEYQIOGNSAENENNSW-TRVAFAGLKFQDVGSEFDYGR--N 114
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 43 KIGFKGEGDGLNGKKAIMOLE---QKASLAGTNSGWNROSFTGLK---GGGTYVAGN 95
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 115 YGVVY-----DYSMTVDLPEFGDGYGSDNFMQOGRNFGATYRNTDFGL-----VDGL 164
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 96 LNTVLDSDGQNVANM-----ESSGNT-----EDVGLGTLGRVESR 131
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 165 NFAVQYQKNGNSGEGFTSGV---TNNGRDA-----LRONGDVGSGITVDYEGFGLG 215
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 132 EISVRVD---SPVAFGSSGQYVPRDANDVDYKHTKRSRESYHAGLKYENAGFPQG 187
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 216 GAISSSK---RTDAQNTAAYTNGDRAETV-----TGGLKYDANNIY--LAAQYTOTYN 264
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 188 YASSFAKYADLNDADAEVAVNTANAHFVKDYQVHRVAG--YDANDLYSVVAGQYEAANK 245
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 265 ATRVAGSL-GWANKAQNFEAAYQFDEGLRPSLAYLOS--KGRNIG--RCYDDEDILIKYV 319
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 246 -NEVGSTKGGKKHEDQTVAAALAYRFG-NYTPRVSYAHGFRKAYNGVKANDAYQYDQYI--- 300
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 320 DVGATYYFNKNNMSTYV 335
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```



```

: REFERENCE/DOCKET NUMBER: 1438.0060002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 363 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-798-760-6

Query Match      7.2%  Score 140.5;  DB 3;  Length 363;
Best Local Similarity 25.6%  Pred. No. 0.00016;
Matches  81;  Conservative 38;  Mismatches 116;  Indels  81;  Gaps  21;

QY  58  RLKRGGEQVYDQLTGYQWMEYQIDGSAENNNNSW-TRVAFAGLKFDVGSFDDGR--N 114
      ::||||: : : : | | | | | : : : | | | | | : : : | | | | |
Db   64  KIGFGEGEDLNGMAIMWLE---QKASIGATGNSGNGRQSTIGLK---GGFTVVRGN 116
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
QY  115  YGVVY-----DVTGWTVDLPFGGDTYSDNFMOGRNGFATRYNTDFGL-----VQGL 164
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db   117  LNTVLYGSDGVVNM-----ESGNT-----EDVLGLGTIGRVESR 152
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
QY  165  NFAVOYQKNGNPSGEGFTGCV---TNGGDA-----LRONGDVGGSITYDYEGFGIG 215
      : : | : : | | : : | | : : | | : : | | : : | | : : | |
Db   153  EISVRYD---SPVAFGSGSVQVYPRDNANDVDKXKHTKSSRESYHAGLKYEAGFPGQ 208
      : : | : : | | : : | | : : | | : : | | : : | | : : | |
QY  216  GAISRSK-----RTDAONTAAIYIGNDRAEY-----TGLKYDANNIT--LAAQYTQYTN 264
      : : | : : | | : : | | : : | | : : | | : : | | : : | |
Db   209  YAGSPAKYADINTLAERAVAVNTANHPVKDYQVHRVAVG--YDANDLYVSVAQGYEAAKN 266
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
QY  265  ATRPGSL-GMAKNQKNEFAVAVOYQDFGLRPSLAYLQS-KGKNLG---RGYDEDEILKYV 319
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db   267  NEVGSTGKKHHEQTQVAATATATPRG-NVTPRVSTAHGFAKAKVNGVKANQYDQYI--- 321
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
QY  320  DVGATYYFNKNMSTYV 335
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db   322  -VGADYDESKRTSALV 336
      | | | | | : : : | | | | | : : : | | | | | : : : | | | | |

RESULT 15
PCT-US94-08327-6
: Sequence 6, Application PC/TUS9408327
: GENERAL INFORMATION:
: APPLICANT: The Rockefeller University
: APPLICANT: 1230 York Avenue
: APPLICANT: New York, New York 10021
: APPLICANT: United States of America
: APPLICANT: 12103 Indian Creek Court
: APPLICANT: Beltsville, Maryland 20705
: APPLICANT: United States of America
: APPLICANT: Tai, Joseph Y.
: APPLICANT: Qi, HuiLin L.
: APPLICANT: Liang, Shu-Mei
: APPLICANT: Hironowski, Lucjan J.J.
: APPLICANT: Pullen, Jeffrey K.
: TITLE OF INVENTION: Method for the High Level
: TITLE OF INVENTION: Expression,
: TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
: TITLE OF INVENTION: Group B
: TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Ave., Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438, 006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08327-6

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Query Match	7.2%;	Score 140.5;	DB 5;	Length 363;
Best Local Similarity	25.6%;	Pred. No. 0.00016;		
Matches 81;	Conservative	38;	Mismatches 116;	Indels 81;
			Gaps	21.

QY	58	RLGRGETQVTDLTGTYGOMEYOLOGNSAENENNSW-TRVAFAGLKFDQVGSFEDYGR--N	114
		:	
Db	64	KIGRGGQDLDLNGKMAIMQLE---QKASLGTAGNSGWRQSPHGLK-----GGFGTVIRAGN	116
QY	115	YGVVY-----DYTSKTDVLPFEGGDTYSDDNFMOQRGNFGATYRTDFFGL-----VDGL	164
		: : : : : : : : :	
Db	117	LNTFLKDSGDVNVNVA-----EGSNT-----EDVLGLGTIGRVESR	152
QY	165	NFAVOYQCKNKNPSEGEFTSGV-----TNNGRDA-----LRQNGDVGSSITPYDYGFGIG	215
Db	153	EISVRYD---SPVAFGSGSVQVYPRDNANDVDKRYKTKSSRESYHAGLKYEAGFFGQ	208
		: : : : : : : : :	
QY	216	GAISSSK---RTQAQNTAAIYIGNDRAETV-----TGGLKYDANNIY--LAAQYTOTYVN	264
		: : : : : : : : :	
Db	209	YAGSFPAKADLNTDAERAIVNTANHPKDYQVHRVAG--YDANDLYVSAGVYEAKN	266
QY	265	ATRVGSL-GMANKAKNFEAVALQYQDFGLRSLAYLQS-KGKNLG---RGYDDEDILKYV	319
		: : : : : : : : :	
Db	267	-NEVSGTSGKKHEQTVAVATAAYRFG-NVTPRVSYAHGFFKAKVNGVKDANYQDOVI---	321
QY	320	DVGATYTYFNKMSITYV	335
		: : : :	
Db	322	-VGADYDFSKRTTSALV	336

Search completed: August 21, 2001, 20:58:50
Job time: 65 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:40 ; Search time 20.32 Seconds
(without alignments)
1094.931 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 1953
Sequence: 1 MKSKYLLALLIPALLAAGAAH.....TRDAGINTDNLVALGLVYQF 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A_Geneseq_0601.*
1: /SID8/gcgdata/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/AA1981.DAT.*
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17: /SID8/gcgdata/geneseq/AA1996.DAT.*
18: /SID8/gcgdata/geneseq/AA1997.DAT.*
19: /SID8/gcgdata/geneseq/AA1998.DAT.*
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21: /SID8/gcgdata/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	20	AAV42549
2	1914	98.0	367	20	AAV34058
3	1914	98.0	367	21	AAV57356
4	1285	65.8	377	20	AAV34057
5	1285	65.8	377	21	AAV57355
6	1104	56.5	362	20	AAV42550
7	1078.5	55.2	323	20	AAV34056
8	1078.5	55.2	323	21	AAV57354
9	1027	52.6	340	17	AAW92998
10	226.5	11.6	89	18	AAW27781
11	187.5	9.6	353	20	AAV26025

12	176	9.0	362	10	AAW90098	P2 antigen of Haem
13	174	8.9	343	20	AAV26024	OmpH protein of Pa
14	171	8.8	353	20	AAV26023	OmpH protein of Pa
15	164.5	8.4	361	11	AAW05999	P2 gene product of
16	164.5	8.4	361	16	AAW66877	H. influenzae P2 e
17	161.5	8.3	350	18	AAW21678	Haemophilus influe
18	148.5	7.6	350	13	AAW27484	Protein IB of N. g
19	147.5	7.6	350	10	AAW90100	Class II outer mem
20	146	7.5	353	11	AAW60308	Gonococcal porin-5
21	145.5	7.5	372	16	AAW66607	Mature class 2 por
22	140.5	7.2	342	16	AAW70763	Neisseria meningit
23	140.5	7.2	342	18	AAW21742	Fusion Class 2 por
24	140.5	7.2	363	16	AAW70764	Neisseria meningit
25	140.5	7.2	363	18	AAW21743	Class IB outer mem
26	132	6.8	328	11	AAW60306	P3 gene product of
27	130.5	6.7	341	11	AAW07043	A surface protein
28	128.5	6.6	589	20	AAW23745	Class IA outer mem
29	127.5	6.5	326	11	AAW06037	PNV-2 fusion const
30	127.5	6.5	363	16	AAW66878	Class I OMP derive
31	127.5	6.5	373	11	AAW06043	H. influenzae prot
32	126.5	6.5	342	16	AAW66879	Class I OMP derive
33	126.5	6.5	342	16	AAW66880	Meningococcal pl.7
34	126.5	6.5	366	11	AAW06044	Class I OMP derive
35	125.5	6.4	373	14	AAW37728	Class I OMP derive
36	125	6.4	368	11	AAW06042	Class I OMP derive
37	124.5	6.4	341	11	AAW07042	P3 gene product of
38	124.5	6.4	511	17	AAW95012	C. difficile toxin
39	124.5	6.4	511	17	AAW75371	C. difficile toxin
40	124.5	6.4	608	17	AAW95013	C. difficile toxin
41	124.5	6.4	609	17	AAW95018	C. difficile toxin
42	124.5	6.4	611	17	AAW75372	C. difficile toxin
43	124.5	6.4	2366	17	AAW95011	Clostridium diffic
44	124.5	6.4	2366	19	AAW68388	Class I outer memb
45	121	6.2	373	11	AAW06035	

ALIGNMENTS

RESULT 1	
AAV42549	standard; Protein; 367 AA.
AC	AAV42549;
DT	20-DEC-1999 (first entry)
XX	E. coli wild-type ompC protein.
DE	
XX	Bacteria: attenuation; deletion; mutant; vaccine; immune response;
KW	Gram negative; infection; diarrhoea; food poisoning; typhoid;
KW	salmonellosis; gonorrhoea; gastroenteritis; whooping cough.
XX	
OS	Escherichia coli.
XX	
PN	WC0949026-A1.
XX	
PD	30-SEP-1999.
XX	
PF	25-MAR-1999; 99WO-GB00935.
XX	
PR	25-MAR-1998; 98GB-0006449.
XX	
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.
XX	
PI	Chaffield SN;
XX	
DR	WPI: 1999-580447/49.
XX	
DR	N-PSDB; AA22885.
XX	
PT	New attenuated bacteria useful as vaccines for protecting against
PT	infections
XX	

RESULT 3

AA57356 standard; Protein; 367 AA.

AA57356;

13-JUN-2000 (first entry)

E. coli outer membrane protein c precursor.

Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb;

PANCA; perinuclear anti-neutrophil cytoplasmic antibody;

histone H1; outer membrane protein c precursor.

Escherichia coli.

US6033864-A.

07-MAR-2000.

12-MAR-1998; 98US-0041889.

12-APR-1996; 96US-0057846.

11-APR-1997; 97US-0837058.

(REGC) UNIV CALIFORNIA.

Cohavy O, Braun J;

WPI; 2000-255695/22.

Diagnosing ulcerative colitis or susceptibility, by detecting complex

formation between microbial porin antigen and perinuclear

anti-neutrophil cytoplasmic autoantibodies

Claim 1; Fig 10; 49pp: English.

The invention provides a method for diagnosing ulcerative colitis in a

subject suspected of having inflammatory bowel disease. The method

comprises reacting a patient sample with a porin antigen that is

immunologically reactive with PANCA (perinuclear anti-neutrophil

cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex

as indicative of ulcerative colitis. The method is used to diagnose

ulcerative colitis or susceptibility to it. The present sequence

represents a E. coli outer membrane protein c precursor.

Sequence 367 AA;

Query Match

Best Local Similarity 98.0%; Score 1914; DB 21; Length 367;

Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 M K S K V L A L L I P A L I A A G A A H A E Y N K D G N K L D Y G V D G L H F S D N K D V D G D O T Y M R L G 60

1 m k v t w d l p e f g d t y g s d n f m o o r n f a t y r n t d f f g l v d g l n f a v y q y g k n g n p s g e 180

121 v t s w t d v l p e f g d t y g s d n f m o o r n f a t y r n t d f f g l v d g l n f a v y q y g k n g n p s g e 180

181 g f t s g v t n n g d a l r o n g d v g s i t y d y e g f i g a l i s s s k r t d a o n t a a y i c n g d r a e 240

181 g f t s g v t n n g d a l r o n g d v g s i t y d y e g f i g a l i s s s k r t d a o n t a a y i c n g d r a e 240

241 t y t g i k a k d a n n i t l a o y r o t y n a t r v g s l g a n k a n k o n f e a v a o y g e d f g l r s l a y l q 300

Db 241 tytgikakdannitlaoyrotynatrvgslganakankafavayqdfdgflrslaylq 300

Qy 301 SKGRNLGRGYDDEDILKRVYDVGATYFENKNNSTYVDYKINLDDNQFTRDAGINTDNIYA 360

Db 301 skgrnlgrgyddedilkyvdvgatcyfknkstvydykinlddnqftrdagintdniva 360

Qy 361 LGLVYQF 367

Db 361 lglvyqf 367

RESULT 4

AA574057 standard; protein; 377 AA.

AA574057;

23-NOV-1999 (first entry)

E. coli outer membrane protein F precursor.

Ulcerative colitis; histone; H1-like antigen; porin antigen;

Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;

diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;

outer membrane protein F precursor.

Escherichia coli.

WO945955-A1.

16-SEP-1999.

12-MAR-1999; 99WO-US05492.

12-MAR-1998; 98US-0041889.

(REGC) UNIV CALIFORNIA.

Braun J, Cohavy O;

WPI; 1999-551215/46.

Use of histone H1, porin or Bacteroides antigens as targets for the

diagnosis, prevention and treatment of ulcerative colitis

Claim 8; Fig 11; 134pp: English.

The invention provides a method for the diagnosis, prevention and

treatment of ulcerative colitis (UC) using histone H1-like antigen, a

porin antigen or a Bacteroides antigen as a target antigen. The novel

method of diagnosing UC in a subject suspected of having inflammatory

bowel disease (IBD) comprises: (1) obtaining a sample from the subject;

(2) contacting the sample with a histone H1-like antigen, or perinuclear

anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a

complex of the histone H1-like antigen, or the PANCA-reactive fragment,

and antibody to the histone H1-like antigen; and (3) detecting the

presence or absence of the complex; where the presence of the complex

indicates that the subject has UC. The PANCA-reactive histone H1-like

antigen, porin antigen and Bacteroides antigen are useful in the

diagnosis, prevention and treatment of UC. The methods can also be used

for identifying agents useful for treating UC. The present sequence

represents a E. coli outer membrane protein F precursor.

Sequence 377 AA;

Query Match

Best Local Similarity 65.8%; Score 1285; DB 20; Length 377;

Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;

1 M K S K V L A L L I P A L I A A G A A H A E Y N K D G N K L D Y G V D G L H F S D N K D V D G D O T Y M R L G 60

1 m k s k v l a l l i p a l i a a g a a h a e y n k d g n k l d y g v d g l h y f s d n s a k d g d q s y a r i g 60

DT 13-JUN-2000 (first entry)
 XX
 DE E. coli outer membrane protein F precursor.
 XX
 KM ulcerative colitis; inflammatory bowel disease; porin antigen; Mab;
 KM PANCA; perinuclear anti-neutrophil cytoplasmic antibody;
 KM histone H1; outer membrane protein F precursor.
 XX
 OS Escherichia coli.
 XX
 PN US6033864-A.
 PD 07-MAR-2000.
 XX
 PF 12-MAR-1998; 98US-0041889.
 XX
 PR 12-APR-1996; 96US-0057846.
 PR 11-APR-1997; 97US-0837058.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Cohavy O, Braun J;
 XX
 DR WPI; 2000-255695/22.
 XX
 PT Diagnosing ulcerative colitis or susceptibility, by detecting complex
 PT formation between microbial porin antigen and perinuclear
 PT anti-neutrophil cytoplasmic autoantibodies -
 XX
 PS Claim 1; Fig 10; 49pp; English.
 XX
 CC The invention provides a method for diagnosing ulcerative colitis in a
 CC subject suspected of having inflammatory bowel disease. The method
 CC comprises reacting a patient sample with a porin antigen that is
 CC immunologically reactive with PANCA (perinuclear anti-neutrophil
 CC cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. The present sequence
 CC represents a E. coli outer membrane protein F precursor.
 XX
 SO Sequence 323 AA;

Query Match 55.2%; Score 1078.5; DB 21; Length 323;
 Best Local Similarity 66.2%; Pred. No. 1.2e-78;
 Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MRSKVALLIPALLAAGAAHAAEYVYKDGKLDLYGVGLHFSNKKDVGQTTWRIG 60
 DB 1 mskviallilpallaaagaaevykdgnkldlygvglhfyfsdnakdgqdsyarlg 60
 QY 61 FKRETOVTDLTGYGOMEVYIOGNSAE--NENNSMTRYAFAGLKFODVSGFDRNTGVY 119
 DB 61 fketvtodltygomevniognsaenennsmtryafaglkfodvsgfdrntgvny 120
 QY 120 DVYSMTDVLPEFGSDTY--GSDNFMQORGNFGATRYNTDFEGLVDGLNFAVOYOGKNGNPS 178
 DB 120 dvysmtdvlpefgsdytysdgnfmqorgnfgatryntdfeglvdglnfavoogkngnps 178
 QY 121 diegwtdmlpefgsdytysdgnfmqorgnfgatryntdfeglvdglnfavoogkngnps 176
 DB 121 diegwtdmlpefgsdytysdgnfmqorgnfgatryntdfeglvdglnfavoogkngnps 176
 QY 179 GEGFTSGV--TNNGRDALRONGDGVGGSTYYD--EGFGIGAISSSKRIDAQ--NTAAYT 233
 DB 179 gegftsgv--tnngrdalrongdgvvggstyyd--egfgigaiissksridaq--ntaayt 233
 QY 177 -egasnvgqelungtrdrhngsgvgjstlydlmgfisaagaytssdrtdndynhtaa-- 233
 DB 177 -egasnvgqelungtrdrhngsgvgjstlydlmgfisaagaytssdrtdndynhtaa-- 233
 QY 234 GNGDRAETVYGGIKYDANNIYLAAYTOTYNTATRVGSLG--ANKAONFEAFAVOYQEDFG 291
 DB 234 gngdraetvyygikydannilylaaytotyntatrvvgslg--ankaonfeafaavoqedfg 291
 QY 234 -ggdkdadaaglkkydannyilaaysetrnmrpfsgsdyaavankqntevtagyqtdig 292
 DB 234 -ggdkdadaaglkkydannyilaaysetrnmrpfsgsdyaavankqntevtagyqtdig 292
 QY 292 LRPSLAYLQSKGNL-----GRGYDDED 314
 DB 292 lrpsvflmskgrldhaagadnpgavddk 323

AAW92998
 ID AAW92998 standard; protein; 340 AA.
 XX
 AC AAW92998;
 XX
 DT 19-MAY-1999 (first entry)
 XX
 DE E. coli OmpF porin protein.
 XX
 KM OmpF; porin; amphiphilic alpha-structure; beta-structure; GLUT;
 KM membrane protein; glucose transporter protein; function.
 XX
 OS Escherichia coli.
 XX
 PN WO9618957-A1.
 PD 20-JUN-1996.
 XX
 PF 13-DEC-1995; 95WO-US16126.
 XX
 PR 14-DEC-1994; 94US-0355844.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Cheung M, Czegledy F, Fischbarg J, Iserovich P;
 PI Li J;
 XX
 DR WPI; 1996-300839/30.
 XX
 PT Predicting tendency to form amphiphilic alpha and beta structures -
 PT using a novel algorithm to calculate values for subsequent graphical
 PT analysis to predict protein structure
 XX
 PS Disclosure; Fig 2; 106pp; English.
 XX
 CC This invention describes a novel method for predicting the tendency of
 CC a protein to form either: (a) an amphiphilic alpha-structure or (b) an
 CC amphiphilic beta-structure. The methods are used particularly for
 CC predicting the structure of membrane proteins such as glucose transporter
 CC proteins (GLUTs). They can be used to discern the function of proteins.
 CC They can also be used for the rational design or identification of
 CC compounds which interact with the proteins or to engineer proteins having
 CC particular structures. This sequence represents an Escherichia coli
 CC OmpF porin which is used to illustrate the method of the invention.
 XX
 SO Sequence 340 AA;

Query Match 52.6%; Score 1027; DB 17; Length 340;
 Best Local Similarity 58.4%; Pred. No. 1.8e-74;
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEYVYKNDGKLDLYGVGLHFS-----DNKDYDGDQTYMRGFGGEQVYDQTLGYGQ 76
 DB 22 aeivyknkdgkldlygvglhfs-----dnkdydgdqtymrfgfggeqvdydqltgygq 76
 QY 1 aelyvnykndgkldlygvglhfskngensygnndmtyarlgfgeqtdlnsdltgygq 60
 DB 1 aelyvnykndgkldlygvglhfskngensygnndmtyarlgfgeqtdlnsdltgygq 60
 QY 77 WEQIOGNSAEN---ENNSMTRYAFAGLKFODVSGFDRNTGVYDVYSMTDVLPEFG 133
 DB 77 weqioqnsaen---ennsmttryafaglkfodvsgfdrntgvnydvysmtdvlpefg 133
 QY 61 weynfgnmsegadaqtnktrilaafaglkxadvgstidgrnygvvdalgytdmlpefg 120
 DB 61 weynfgnmsegadaqtnktrilaafaglkxadvgstidgrnygvvdalgytdmlpefg 120
 QY 134 DRYSDNFMQORGNFGATRYNTDFEGLVDGLNFAVOYOGKNGNPSGEGFTSGVTNNGRD- 192
 DB 134 drysdnfmqorgnfgatryntdfeglvdglnfavoogkngnpsgegftsgvtnngrd- 192
 QY 121 dtaysdfffvrgvgyatrynsnffglvgdlnfavgylgk-----nerdt 165
 DB 121 dtaysdfffvrgvgyatrynsnffglvgdlnfavgylgk-----nerdt 165
 QY 193 ALRONGDGVGGSTYYIEGFGIGAISSSKRIDAQNTAAYTNGDAETTYTGLKTDANN 252
 DB 193 alrongdgvvggstyyiebgfgigaiissksridaqntaaytngdaetvtytglktdann 252
 QY 166 arrnsdgyvgysisyeibgfgivgayaadrtlnlge--aqplngkkaeqwalgkxndan 224
 DB 166 arrnsdgyvgysisyeibgfgivgayaadrtlnlge--aqplngkkaeqwalgkxndan 224
 QY 253 IYLAAYTOTYNTATRV-----GSLGWANKAONFEAFAVOYQEDFGLRPSLAYLQSKGNL 307
 DB 253 iylaaytotyntatrv-----gslgwankaonfeafaavoqedfgrpslaylqskgnl 307
 QY 225 iylaanygetrnatpiltntfntsgfanktdvllvaqyqfdgltprslaylqskskakv- 283
 DB 225 iylaanygetrnatpiltntfntsgfanktdvllvaqyqfdgltprslaylqskskakv- 283
 QY 308 RGYDDEDILKYVDVAGATYFENKMSITYVDYKINLND--DNOFTRDAGINFDNIVALGLVYQ 366
 DB 308 rgyddebdlkyyvdvagtayfennkmsityvdykinlnd--dnoftredaginfdnivalglvyq 366

Query Match	Score	DB	Length
Best Local Similarity	59.2%	Pred No. 3.6e-11;	
Query Match	11.6%	Score 226.5;	DB 18; Length 89;

	Matches	45;	Conservative	10;	Mismatches	16;	Indels	5;	Gaps	1
OY	1	MKS	KVLLALLIP	LALAGAAHAEVYNKDGSKLDLYGKVDGLHYFS-----DKMKDVGDOQT	55					
			:::::	::	::	::	::	::	::	
Dd	2	mknrl	lavipallv	agitanaaeylnkdgnkvdlygkavglhxfskngensyggngdmnt	61					
OY	56	YMR	LGEFGTEQVTDLQ	71						
Dd	62	yarl	gfkgelqxnsl	77						
	RESULT	11								
ID	AAY26025									
XX	AAY26025 standard; Protein: 353 AA.									
XX	AAY26025;									
AC										
DT	29-SEP-1999 (first entry)									
XX										
DE	Omph protein of H.influenza porin P2.									
XX										
KW	Outer membrane protein H; omph gene; fowl cholera; molecular sieve;									
KM	Pasteurella multocida X-73; porin; avian; vaccine; veterinary medicine;									
RW	bacterial porin; H.influenzae porin P2.									
XX										
OS	Haemophilus influenzae.									
XX										
PN	WO9929724-A2.									
XX										
PD	17-JUN-1999.									
PF										
XX	08-DEC-1998; 98WO-US25990.									
PR	21-JUL-1998; 98US-0120051.									
XX	08-DEC-1997; 97US-0067957.									
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.									
PI	Glisson JR, Luo Y;									
DR	WPI: 1999-385575/32.									
PT	DNA encoding Pasteurella multocida outer membrane protein H, useful									
PS	for delivering peptide epitopes for vaccines against fowl cholera									
XX	Disclosure; Fig 5; 11pp; English.									
CC	The present amino acid sequence is that of the Haemophilus influenzae									
CC	porin P2. This protein is a bacterial porin, which is a major outer									
CC	membrane protein that is involved in pore formation. They serve as									
CC	molecular sieves that allow polar solutes to pass through, but excludes									
CC	non-polar molecules of comparable sizes. This amino acid sequence shares									
CC	a sequence homology of about 38% to Pasteurella multocida X-73 Omph									
CC	protein. Peptides derived from the P.multocida Omph protein are useful									
CC	in the production of protective vaccines for use in vertebrates in									
CC	particular, for prevention of fowl cholera and for diagnosis in									
CC	veterinary medicine.									
XX										
SQ	Sequence 353 AA;									
	Query Match	9.6%;	Score	187.5;	DB	20;	Length	353;		
	Best Local Similarity	21.9%;	Pred.	No. 2.9e-07;						
	Matches	89;	Conservative	53;	Mismatches	126;	Indels	139;	Gaps	16;
OY	4	KVL	ALLIPALLAAGAHAAEVYNKDGSKLDLYGKV-----	38						
Dd	3	krla	ilivgaTaasaanaavynegtkvclagrsvsiaegstsnrkdkqhgslnrg	62						
OY	39	----	DG---LHFESD---NNDVGDQDYVMRLGFEGFGENGVDPDLGYQGWEHQ	80						
Dd	63	srfn	ikvtmhlmgdyalgyetrfinxldidgneknigsqgstl-----	107						

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OY 81 IQGNSAENENNSMTIRVAFEGJLFDODVSPFDGRNRYGVAVDTSMWDLPEFGDYGSDN 140
Db 108 -----kleyaglgmkeiglealtfglqtklactsted--kxyg--vlekn 150
OY 141 FMOQRG-----FGATY-----RNTDFEGLVDG-LNFVAYOYQK-NGNPSGEG 181
Db 151 yipegnalaytykiglelltgaasyvfgjrnfsdelyeltdkvsnaavgakylannivag 210
OY 182 FTSQGTN-NGRBDALRONGSDGVGSITDYDESGF-----GGAISSKRTQAQMTAAICN 235
Db 211 faygrtnykaqqaktqgvngalacilgjhfdlgljlslsdsgyaktknakhekryivsp 270
OY 236 GDRAE-----TYTGKLYDANNITVLAQAQYQTYVNTATRVSGLSGMANKAQNQNEAVAOYQDF 290
Db 271 gfygylmedtnlgnlkyer-----lnsvdggekvrehavlf 307
OY 291 GLRPSL-----AYLQSKCKNLRGVDDEDILTKYVDVGAITYYF 327
Db 308 gidhklhkvlytleagayarrtnndkqktek-eksvvgvlrvlyf 353

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RESULT	12
AAP90098	
ID	AAP90098 standard; protein; 362 AA

XX	AAP90098;
XX	01-NOV-1989 (first entry)
XX	P2 antigen of Haemophilus influenzae.
XX	Haemophilus influenzae P2 antigen; vaccines; pathogenic type b strains.
XX	Haemophilus influenzae type b.
XX	EP320289-A.
XX	14-JUN-1989.
XX	09-DEC-1988; 88EP-0311691.
XX	10-DEC-1987; 87US-0249482.
XX	(TEXA) UNIV OF TEXAS SYST.
XX	Hansen EJ;
XX	WPI; 1989-174562/24.
XX	DNA encoding Haemophilus influenzae P2 antigen - used for producing immunogenic compns. as vaccines and in diagnostic hybridisation assays.
XX	Disclosure; fig 6; 20pp; English.
XX	P2 antigen of Haemophilus influenzae (see corresp. AAN90033).
XX	Isolated from type b strains, the P2 antigens are used as vaccines CC and to detect P2-specific RNA or DNA. Segments used as antigens include amino acids 21-361, 175-197, 260-275, 296-311, 33-353,
XX	or their functional equivalents.
Sequence	362 AA;
50	

Query Match	9.0%;	Score 176;	DB 10;	Length 362;
Best Local Similarity	24.1%;	Pred. No. 2.5e-06;		
Matches 90;	Conservative 53;	Mismatches 145;	Indels 86;	Gaps 16;

QY 4 KVALLLIPALLAAGAHAIAEVYKKDGNKIDL YGKVDGLHYFSDNKDVSDQTY ----- 56
| | | | | | | | | | : : : : : | | | :
Db 3 ktlaallivgafaasanaavynnegtnvelgrrlsllaegsnstvnngkqghalrng 62

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Oy 57 -MRGFEKETQVTLQTLNGYQWMEYQIQGNSNENNNNSM----TFVAFAGLKFDQVSGFDY 111
Db 63 gsrfltkathmfqgIyaqgyletrfctkasengsnfdgatskyavvltlgnkafgevkI 122
Oy 112 GRNGVGVVDVTSMTDVLPEFGFDYGGSDNFMQQRGN--FGATYRNTDPEFGLVDGILNFAVQY 170
Db 123 graktiadgitsaed--keyg--vlnmsdyipetsgnvgytffgid--qlvlgany----- 172
Oy 171 QGKNGNPSEGEFTSGVTNNGRDALRQNGDVGSGSITYDYEGFGIGAISSSKRTDAQNTA 230
Db 173 -----llaqrregakg-----enkrpnudkage 194
Oy 231 AYIG--NGBRAEYTYTGGKRTDANNITLLAAYOTF---YNATRVGSLGMANKAO--NFEA 282
Db 195 vrlengingdy-----gakydandivaklgyatnykhesd-----ehkqqlngvla 243
Oy 283 VAQYQF--DFGLRPLSLATVQSGSKGNLNGGQYDDEDLTKVVDGATYFENKKNSTYVDYKI-- 339
Db 244 tlygrfscdglivlidsqyaktknykikhekr---yivspgfygylmedtnvgnfkfyer 300
Oy 340 NLLDLNOFTRDAGI 353
Db 301 tsvdgakektiregav 314

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RESULT	13
AAV26024	
ID	AAV26024 standard; Protein; 343 AA.

AC	AAV26024;
XX	
DT	29-SEP-1999 (first entry)

DE OmpH protein of *Pasteurella multocida* P-1059.
XX
KM Outer membrane protein H; ompH gene; fowl cholera; molecular sieve
KM *Pasteurella multocida* P-1059; porlin; vaccine; veterinary medicine;
KM bacterial porlin; *H. influenzae* porlin P2; avian.
XX
XX *Pasteurella multocida*.
DS

FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label="Signal_peptide"
FT		/note="Hydrophobic amino acids"
FT	Protein	21..343
FT		/note="mature Omph protein"
FT	Cleavage-site	7..9
FT		/note="Found within signal_peptide"
FT	Cleavage-site	9..11
FT		/note="Found within signal_peptide"
FT	Cleavage-site	12..14
FT		/note="Found within signal_peptide"
FT	Cleavage-site	18..20
FT		/note="Found within signal_peptide"

PN W099929724-A2.

PD 17-JUN-15

PF 08-DEC-1998; 98WO-US25990.

PR 21-JUL-1998; 98US-0120051.

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DR N-PSDB; AAX80610.

PT DNA encoding *Pasteurella multocida* outer membrane protein H, useful

